

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 20:16:55 ; Search time 1457.41 Seconds
(without alignments)
11926.532 Million cell updates/sec

Title: US-10-764-316-7
Perfect score: 2493
Sequence: 1 ccggcgccggcgccggcgag.....aaataaacttttaaaactcc 2493

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 524920 seqs, 3486124231 residues

Word size : 1
Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2493	100.0	2493	6	ABA02398 Human hea
2	502	20.1	2279	14	ABE54684 DNA encod
3	495	19.9	2361	3	AAF18262 Lung canc
4	484	19.4	2336	12	ADE77038 Human cDN
5	431	17.3	2962	8	ABX622981 Human act
6	431	17.3	2962	13	ADI161704 Human cDN
7	431	17.3	2962	14	AEA43869 Human cDN
8	429	17.2	531	12	ADP66225 Human cDN
9	329	13.2	2492	6	ABL68660 Kidney ca
10	329	13.2	2492	6	ABK84553 Human cDN
11	329	13.2	2492	8	ACA64921 Human HSP
12	329	13.2	2492	15	AEP92617 Human hea
13	283	11.4	1932	6	ABA96361 Human sch
14	283	11.4	1932	10	ADD18651 Human dis
15	283	11.4	1932	12	ADP12821 Reference
16	283	11.4	1932	13	ADP14394 Human NF-
17	283	11.4	1932	13	ADP22911 PRO polyp
18	283	11.4	1932	14	ADV42954 Human psy

19	283	11.4	1932	14	ADX06581	Adx06581 Cyclin-de
20	259	10.4	1001	13	ADQ80920	Adq80920 Human phe
21	187	7.5	445	13	ADU13608	Adu13608 Solid tum
22	154	6.2	1001	13	ADQ80919	Adq80919 Human phe
23	120	4.8	968	11	ADI31786	Adi31786 Human cDN
24	120	4.8	968	13	ADS83853	Ads83853 Human lym
25	120	4.8	968	15	AEF92618	Aef92618 Human hea
26	102	4.1	1280	14	ADV97672	Adv97672 Human hea
27	100	4.0	286	2	AAV21143	Aav21143 Human hsp
28	100	4.0	469	2	AAV56356	Aav56356 Human hea
29	100	4.0	469	12	ADL32452	Adl32452 Human hea
30	100	4.0	469	14	ABE68778	Aeb68778 Human min
31	100	4.0	550	4	AAQ01683	Aas01683 Human hea
32	100	4.0	592	8	ACA61270	Aca61270 Human hea
33	100	4.0	592	9	ACF35886	Acf35886 Human hea
34	100	4.0	714	8	ACC43397	Acc43397 5' UTR of
35	91	3.7	445	13	ADU13658	Adul3658 Solid tum
36	85	3.4	159	3	AAC09982	Aac09982 Human sec
37	76	3.0	475	9	ACH44271	Ach44271 Human foe
38	75	3.0	376	14	ACL54045	Ac154045 Human col
39	71	2.8	2386	2	AAT38809	Aat38809 Marmoset
40	60	2.4	60	6	ABN38808	Abn38808 Human spl
41	58	2.3	119	3	AAA94741	Aaa94741 Human HSP
42	50	2.0	50	6	ABZ02264	Abz02264 Human leu
43	50	2.0	50	12	ADP12652	Adp12652 50-mer ol
44	48	1.9	768	6	ABQ34182	Abq34182 Oligonuc
45	48	1.9	768	6	ABQ34183	Abq34183 Oligonuc

ALIGNMENTS

RESULT 1
ABA02398 standard; DNA; 2493 BP.

AC ABA02398;
DT 26-FEB-2002 (first entry)

DE Human heat shock protein HSPA7-encoding DNA.

KW Human; heat shock protein; HSPA7; SCZ gene; chromosome 1q22;
KW schizophrenia; schizoaffective disorder; susceptibility; diagnosis;
KW polymorphic marker; linkage disequilibrium; APOA2; FCER1G; FCGR2A;
KW D1S2675; B22624T; neuroleptic; gene therapy; drug screening;
KW in utero screening; ds.

OS Homo sapiens.

PN WO200180718-A2.

XX 01-NOV-2001.

PF 23-APR-2001; 2001WO-US013073.

PR 21-APR-2000; 2000US-0199114P.

PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.

PI Brzustowicz LM, Bassett AS;

DR WPI; 2002-049235/06.

XX Diagnosing susceptibility to schizophrenia in a patient, involves
PT detecting polymorphic marker allele within chromosome segment 1q22
PT bordered by D1S2705 and D1S1679 and linked to variant form of SCZ DNA
segment.

PS Claim 19; Page 64-66; 77pp; English.

CC This sequence represents DNA encoding the human heat shock protein HSPA7.
The HSPA7 gene is located on chromosome 1q22, a region thought to be

CC associated with schizophrenia and the closely related schizoaffective
CC disorder. The invention identifies the HSPA7 gene as an SCZ gene, a
CC variant form of which is associated with a schizophrenia phenotype. The
CC invention relates to a novel method of diagnosing a patient's
CC susceptibility to schizophrenia. The method involves determining the
CC presence of an allele of a polymorphic marker linked to a variant form
CC of an SCZ gene within a segment of chromosome 1q22 bordered by D1S2705 and
CC D1S1679. The polymorphic marker allele is in phase with the variant form
CC of SCZ, and its presence indicates a susceptibility to schizophrenia and
CC related disorders. The polymorphic marker is APOA2, FCER1G, FCER2A,
CC D1S2675, or preferably B426K24T. The invention also relates to a method
CC for determining an alteration in an SCZ promoter sequence, where the
CC alteration is associated with a schizophrenic condition, and a method for
CC assessing a test compound for its ability to modulate the activity of an
CC SCZ protein. The methods of the invention are useful for diagnosing
CC schizophrenia or schizoaffective disorder, or a susceptibility to these
CC conditions in a patient using a saliva, blood or buccal mucosal cell
CC sample. The HSPA7 proteins and nucleotides have neuroleptic activity and
CC may be used in gene therapy, and HSPA7 protein modulating compounds may
CC be useful in the treatment of schizophrenia and related disorders. The
CC invention also provides a highly accurate assay for in utero screening of
CC foetuses for the presence of a variant SCZ allele, which will enable the
CC administration of appropriate treatment at an early stage
XX
SQ Sequence 2493 BP; 554 A; 676 C; 794 G; 469 T; 0 U; 0 Other;

Query Match 100.0%; Score 2493; DB 6; Length 2493;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGCGGGCGGGGAGGCTCTCGACTGGCGGGAGGTGCGGAGGTTGCGGCG 60
DB 1 CCCGGCGGGCGGGGAGGCTCTCGACTGGCGGGAGGTGCGGAGGTTGCGGCG 60
QY 61 GCGGGGTGCGGAGGTGCAAAAGGATGAAAGCCCGTGGAGCGGAGCTGAGCAGATCCG 120
DB 61 GCGGGGTGCGGAGGTGCAAAAGGATGAAAGCCCGTGGAGCGGAGCTGAGCAGATCCG 120
QY 121 AGCGGGGTGCGGCGAGAGAAACCCGAGGGAGAGCTCACTGCTGAGCGCCCTCGACGG 180
DB 121 AGCGGGGTGCGGCGAGAGAAACCCGAGGGAGAGCTCACTGCTGAGCGCCCTCGACGG 180
QY 181 GCGAGGCGCAGAGCCTCGTGGCTCCAGGATCCGAGCATCCGAGAGGCTTCAGCCATGCGAGC 240
DB 181 GCGAGGCGCAGAGCCTCGTGGCTCCAGGATCCGAGCATCCGAGAGGCTTCAGCCATGCGAGC 240
QY 241 CCCAGGGAGCTCGCGGTGGGCATCGACTGGGCAACCACTACTCGTGGGCGGTGT 300
DB 241 CCCAGGGAGCTCGCGGTGGGCATCGACTGGGCAACCACTACTCGTGGGCGGTGT 300
QY 301 TCAGCAGGGCCGCTGGAGATCCTGGCCAA CGACAGGGGCAACCGCACCGCCAGCTA 360
DB 301 TCAGCAGGGCCGCTGGAGATCCTGGCCAA CGACAGGGGCAACCGCACCGCCAGCTA 360
QY 361 CGTGCCCTTACCGACACCGAGCGCTGGTGGGACCGGCGCAAGAGCCAGGCGGCCCT 420
DB 361 CGTGCCCTTACCGACACCGAGCGCTGGTGGGACCGGCGCAAGAGCCAGGCGGCCCT 420
QY 421 GAAACCCCAACACCGTGTTCGATGCCAAGGGCTGATCGGGCGCAAGTTCGCGGACAC 480
DB 421 GAAACCCCAACACCGTGTTCGATGCCAAGGGCTGATCGGGCGCAAGTTCGCGGACAC 480
QY 481 CACGCTGAGTCCGACATGAAGCATGTGGCCCTTCCAGGTGGTGGAGGCGGCAAGCC 540
DB 481 CACGCTGAGTCCGACATGAAGCATGTGGCCCTTCCAGGTGGTGGAGGCGGCAAGCC 540
QY 541 CACGCTGAGTCCGACATGAAGCATGTGGCCCTTCCAGGTGGTGGAGGCGGCAAGCC 600
DB 541 CACGCTGAGTCCGACATGAAGCATGTGGCCCTTCCAGGTGGTGGAGGCGGCAAGCC 600
QY 601 CATGTGCTGAGCAAGATGAAGGAGACGGCCAGGCGTACCTGGGCCAGCCCGTGAAGCA 660
DB 601 CATGTGCTGAGCAAGATGAAGGAGACGGCCAGGCGTACCTGGGCCAGCCCGTGAAGCA 660

QY 661 GGCAGTATCACCGTCCCACTATTTTCACTAACTCGCAGCGCCAGGCCACCAAGGAGCG 720
DB 661 GGCAGTATCACCGTCCCACTATTTTCACTAACTCGCAGCGCCAGGCCACCAAGGAGCG 720
QY 721 GGGGGCCATCGCGGGGCTCAAGGTGCTGCCGATCATCAATGAGGCCACGGCAGCAGCAT 780
DB 721 GGGGGCCATCGCGGGGCTCAAGGTGCTGCCGATCATCAATGAGGCCACGGCAGCAGCAT 780
QY 781 GGCCTATGGCTGAGACCGGCGGGCGCGGAAAGCGCAACGTGCTCATTTTGTGACTGGG 840
DB 781 GGCCTATGGCTGAGACCGGCGGGCGCGGAAAGCGCAACGTGCTCATTTTGTGACTGGG 840
QY 841 TGGGGGCACTTCGATGTGCGGTCTCTCCATTTGACGCGGTGCTTTGAGGTGAAGC 900
DB 841 TGGGGGCACTTCGATGTGCGGTCTCTCCATTTGACGCGGTGCTTTGAGGTGAAGC 900
QY 901 CACTGCTGGAGATACCCACCTGGGAGGAGAGGACTTCGACAAACCGGCTCGTGAACCACTT 960
DB 901 CACTGCTGGAGATACCCACCTGGGAGGAGAGGACTTCGACAAACCGGCTCGTGAACCACTT 960
QY 961 CATGGAAGAATTCCGGCGGAAGCATGGGAAGGACTGAGCGGGAAACAAGCGTCCCTGCG 1020
DB 961 CATGGAAGAATTCCGGCGGAAGCATGGGAAGGACTGAGCGGGAAACAAGCGTCCCTGCG 1020
QY 1021 CAGGCTGGCAGACGCTGTGAGCGCGCAAGCGCACCCCGTCTCCAGACCCAGGCCAC 1080
DB 1021 CAGGCTGGCAGACGCTGTGAGCGCGCAAGCGCACCCCGTCTCCAGACCCAGGCCAC 1080
QY 1081 CCTGAGATAGACTCCCTGTTTCAGAGGCGTGGACTTCTACAAGTCCATCACTCGTGCCG 1140
DB 1081 CCTGAGATAGACTCCCTGTTTCAGAGGCGTGGACTTCTACAAGTCCATCACTCGTGCCG 1140
QY 1141 CTTTGAAGAACTGTGCTCAGACCTTTCCGAGCACCCCTTGAGCGCGTGGAGAGGCGCCT 1200
DB 1141 CTTTGAAGAACTGTGCTCAGACCTTTCCGAGCACCCCTTGAGCGCGTGGAGAGGCGCCT 1200
QY 1201 GCGGGATGCCAAGCTGACAAAGCCCGATTCATGACTTCTGCTGGGGGAGGGCTCCA 1260
DB 1201 GCGGGATGCCAAGCTGACAAAGCCCGATTCATGACTTCTGCTGGGGGAGGGCTCCA 1260
QY 1261 CTGCGATCCCCAAGGTGAGAAAGTTGCTGACAGGACTTCTTCAACGCGCAAGAGCTGAACA 1320
DB 1261 CTGCGATCCCCAAGGTGAGAAAGTTGCTGACAGGACTTCTTCAACGCGCAAGAGCTGAACA 1320
QY 1321 AGAGCATCAACCCCTGATGAGGCTGTGGCTATGGGCTGTGCTGAGCGCGCGCTGTGGA 1380
DB 1321 AGAGCATCAACCCCTGATGAGGCTGTGGCTATGGGCTGTGCTGAGCGCGCGCTGTGGA 1380
QY 1381 TGGGGGCAATGTGAGAAAGTGCAGGATCTCTGCTGCTGGATGTGGCTCCCTGTCTC 1440
DB 1381 TGGGGGCAATGTGAGAAAGTGCAGGATCTCTGCTGCTGGATGTGGCTCCCTGTCTC 1440
QY 1441 TGGGGCTGGAGACAGCAGGTGGGTGATGACACGCTGATCCAGAGGAACGCCATATCC 1500
DB 1441 TGGGGCTGGAGACAGCAGGTGGGTGATGACACGCTGATCCAGAGGAACGCCATATCC 1500
QY 1501 CCACCAAGCAGACCCAGATTTTCAACCTACTCGGACAAACAGCCTGGGGTCTTCATCC 1560
DB 1501 CCACCAAGCAGACCCAGATTTTCAACCTACTCGGACAAACAGCCTGGGGTCTTCATCC 1560
QY 1561 AGGTGATGAGGTTGAGAGGCGCATGACCAAGGACAAACCTGCTGGGGGCTTTGAAC 1620
DB 1561 AGGTGATGAGGTTGAGAGGCGCATGACCAAGGACAAACCTGCTGGGGGCTTTGAAC 1620
QY 1621 TCATTGGCATCCCTCGTCCCCCATGAGAGTCCCCCAAGATAGAGTACGTTTGAATTG 1680
DB 1621 TCATTGGCATCCCTCGTCCCCCATGAGAGTCCCCCAAGATAGAGTACGTTTGAATTG 1680
QY 1681 ATGCTAATGGCATCCTGAGCGTGAAGCCACTGACAGGAGCACAGGTAAAGGCTAAACA 1740
DB 1681 ATGCTAATGGCATCCTGAGCGTGAAGCCACTGACAGGAGCACAGGTAAAGGCTAAACA 1740

QY 1741 TCACCAATGACAGGGCGGCTGAGCAAGGAGGAGTGGAGAGATGGTTTCATGAAGCCG 1800
Db 1741 TCACCAATGACAGGGCGGCTGAGCAAGGAGGAGTGGAGAGATGGTTTCATGAAGCCG 1800
QY 1801 AGCAGTACGGGGCTGAGGATGAGGCCAGAGGGGACAGATGGCTGCAAAAATCTCGGTGG 1860
Db 1801 AGCAGTACGGGGCTGAGGATGAGGCCAGAGGGGACAGATGGCTGCAAAAATCTCGGTGG 1860
QY 1861 AGGCCCATGTTCTTCATGTGAAGGTTCTTTTCAAGAGGAAAGCCTTAGGGCAAGATTC 1920
Db 1861 AGGCCCATGTTCTTCATGTGAAGGTTCTTTTCAAGAGGAAAGCCTTAGGGCAAGATTC 1920
QY 1921 CCGAAGGACAGGCGCAAGTGCAGACAAAGTGTCAAGAGTCTTGGCTGCTGAGC 1980
Db 1921 CCGAAGGACAGGCGCAAGTGCAGACAAAGTGTCAAGAGTCTTGGCTGCTGAGC 1980
QY 1981 ACAACAGCTGGCAGAGAGGAGTATCAGATCAGAGAGGAGCTGGACCAATCT 2040
Db 1981 ACAACAGCTGGCAGAGAGGAGTATCAGATCAGAGAGGAGCTGGACCAATCT 2040
QY 2041 GTCGCCCATCTTCTCCAGGCTCTATGGGGGGCTGTGTCTCCCTGGGGGAGCAGTTGTA 2100
Db 2041 GTCGCCCATCTTCTCCAGGCTCTATGGGGGGCTGTGTCTCCCTGGGGGAGCAGTTGTA 2100
QY 2101 GCGCTCAGCCACAGGGGACCCAGCACCAGCCGCCCATCATATGAGGAGTTGATGAA 2160
Db 2101 GCGCTCAGCCACAGGGGACCCAGCACCAGCCGCCCATCATATGAGGAGTTGATGAA 2160
QY 2161 TGCGCCCTTCGTATAGTCAAGTGTGACTGTCAAGGCTATGCTATGGCTTCTAGACTG 2220
Db 2161 TGCGCCCTTCGTATAGTCAAGTGTGACTGTCAAGGCTATGCTATGGCTTCTAGACTG 2220
QY 2221 TCTTCTATGATCTGCGCTTCAGAGATGAAGGCTTTGGGGGGTCTTCCCTCCAAAGCTA 2280
Db 2221 TCTTCTATGATCTGCGCTTCAGAGATGAAGGCTTTGGGGGGTCTTCCCTCCAAAGCTA 2280
QY 2281 GAATTTCTTCAGAGATCAAGTCTTTGACTTTTGGGGGAGGCGGTTTCATCC 2340
Db 2281 GAATTTCTTCAGAGATCAAGTCTTTGACTTTTGGGGGAGGCGGTTTCATCC 2340
QY 2341 TCTTCTGCTTCAATAAAGTCAATTAATTTATTAAGCTGTGTGCTGCTTAACTTTAACTTG 2400
Db 2341 TCTTCTGCTTCAATAAAGTCAATTAATTTATTAAGCTGTGTGCTGCTTAACTTTAACTTG 2400
QY 2401 CTTTCACTATATTTTGTGTTTGTATTTTCTTATGATGATGAATTTTGTATGATAATA 2460
Db 2401 CTTTCACTATATTTTGTGTTTGTATTTTCTTATGATGATGAATTTTGTATGATAATA 2460
QY 2461 TAGTTATAGACCTAAATAAATCTTTTAAATCC 2493
Db 2461 TAGTTATAGACCTAAATAAATCTTTTAAATCC 2493

RESULT 2

ID AEB54684 standard; DNA; 2279 BP.

AC AEB54684;

XX 06-OCT-2005 (first entry)

XX DNA encoding human heat shock 70kDa protein 6.

XX heat shock 70kDa protein 6; cancer; neoplasm; gene expression; diagnosis;
KW screening; drug screening; microarray; cytostatic; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 110..2041
CDS /*tag= a

FT /product= "Heat shock 70kDa protein 6"

XX

PN WO2005067650-A2.
XX 28-JUL-2005.
XX 05-JAN-2005; 2005WO-US000518.
XX 06-JAN-2004; 2004US-0534825P.
XX (FARB) BAYER PHARM CORP.
XX Pauloski N, Lynch MJ, Tang L;
PI WPI; 2005-542034/55.
XX P-PSDB; AEB54704.
DR Monitoring or predicting the response to anti-cancer agent comprises
DR determining the gene expression profiles of the sample taken from the
XX patient.
PS Claim 3; SEQ ID NO 10; 91pp; English.
XX The invention relates to a method of monitoring or predicting the
XX response of a patient treated for cancer by administering an anti-cancer
XX agent. The method comprises: (a) determining the level of expression of
XX one or more genes or gene products in a first biological sample taken
XX from the patient prior to treatment with the anti-cancer agent; (b)
XX determining the level of expression of one or more genes or gene products
XX in at least a second biological sample taken from the patient subsequent
XX to the treatment with the anti-cancer agent; and (c) comparing the level
XX of expression of one or more genes (s) or gene products in the second
XX biological sample with the level of expression of one or more genes (s) or
XX gene products in the first biological sample, where a change in the level
XX of expression of one or more genes or gene products in the second
XX biological sample compared to the level of expression of one or more
XX genes or gene products in the first biological sample indicates the
XX efficacy of the treatment with the anti-cancer agent or predicts the
XX response of the patient to anti-cancer agent. Also described are: (1) a
XX method for identifying a compound, useful for treating cancer; (2) a
XX method for providing a patient diagnosis for cancer; (3) a microarray
XX comprising two or more probes corresponding to two or more genes
XX comprising any of the 20 nucleotide sequences given as SEQ ID NOS: 1-20
XX in the specification or comprising two or more polypeptides comprising
XX any of the 20 sequences given as SEQ ID NOS: 21-40 in the specification;
XX and (4) a test kit comprising a primer or probe for measuring the
XX expression level of a nucleic acid selected from SEQ ID NOS: 1-20 or
XX comprising an antibody specific for a polypeptide selected from SEQ ID
XX NOS: 21-40. Also disclosed are methods for screening the effects of a
XX drug on a tissue or cell sample, for discovering novel drugs, for
XX distinguishing between normal and diseases states, and for determining
XX the phenotype of cells. The methods of the invention are useful for
XX obtaining gene expression profiles, and microarrays comprising nucleic
XX acid sequences representing gene expression profiles. In particular, the
XX methods of the invention are useful for monitoring or predicting the
XX response of a patient treated for cancer by administering an anti-cancer
XX agent. The composition and methods are useful for diagnosing and treating
XX cancer. This sequence represents a human polynucleotide sequence that can
XX be used in the method of the invention.
SQ Sequence 2279 BP; 528 A; 637 C; 711 G; 403 T; 0 U; 0 Other;

Query Match 20.1%; Score 502; DB 14; Length 2279;
Best Local Similarity 98.8%; Pred. No. 1.1e-232;
Matches 1422; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 134 GCAGAGAAACCGCAGGGAGAGCCTCCTGCTGAGGCCCTTCGACGGGAGCGGACGCA 193
Db 11 GCAGAGAAACCGCAGGGAGAGCCTCCTGCTGAGGCCCTTCGACGGGAGCGGACGCA 70
QY 194 GCTCCGTGGCTCCAGCATCCGACAGAGCTTCAGCCATCAGGCCGCCCGGAGGCTC 253
Db 71 GCTCCGTGGCTCCAGCATCCGACAGAGCTTCAGCCATCAGGCCGCCCGGAGGCTC 130
QY 254 GCGGTGGGCATCGACCTGGGACCACCTACTCGTGGTGGGCGTGTTCAGCAGGGCGCCG 313

Db 131 CGGTGGGCACTGACCTGGGACCACTACTCTGCTGGGGTGTTCACAGGGCGC 190
Qy 314 GTGAGATCTTGGGCAACGACAGGGCAACCGCACCACTAGTGGCTTCAAC 373
Db 191 GTGAGATCTTGGGCAACGACAGGGCAACCGCACCACTAGTGGCTTCAAC 250
Qy 374 GACACGAGCGGCTGGTGGGGACCGCGCAAGAGCCAGGGCGGCTGAAACCCCAAC 433
Db 251 GACACGAGCGGCTGGTGGGGACCGCGCAAGAGCCAGGGCGGCTGAAACCCCAAC 310
Qy 434 ACCGTGTTGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACCAACCGGTGCGTCG 493
Db 311 ACCGTGTTGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACCAACCGGTGCGTCG 370
Qy 494 GACATGAAGCACTGGCCCTTCCAGTGTGTGAGCGAGCGCGCAAGCGGCGCAAGCGGTGCGGTA 553
Db 371 GACATGAAGCACTGGCCCTTCCAGTGTGTGAGCGAGCGCGCAAGCGGTGCGGTA 430
Qy 554 TGCTACCGGGGAGGACAAGACGTTCTACCCGAGGAGATCTGTCATGGTCTGAGC 613
Db 431 TGCTACCGGGGAGGACAAGACGTTCTACCCGAGGAGATCTGTCATGGTCTGAGC 490
Qy 614 AAGATGAAGGAGACGGCGAGCGGTACCTGGGCCAGCGCGTGAAGCAGCAGTGATCAC 673
Db 491 AAGATGAAGGAGACGGCGAGCGGTACCTGGGCCAGCGCGTGAAGCAGCAGTGATCAC 550
Qy 674 GTGCCACCTATTTTCAGTAATTCGACGCGCGCAGGCGCACCAAGGAGCGGGGGCCATCGCG 733
Db 551 GTGCCCGCTATTTTCAGTAATTCGACGCGCGCAGGCGCACCAAGGAGCGGGGGCCATCGCG 610
Qy 734 GGGCTCAAGTGTCTGCCATCATCAATGAGGCCAGCGCAGCAGCATCGCTATGGGCTG 793
Db 611 GGGCTCAAGTGTCTGCCATCATCAATGAGGCCAGCGCAGCAGCATCGCTATGGGCTG 670
Qy 794 GACCGCGGGGCGGGGAAAGCGCAACCGTGTCTATTTTGGCTGGGGGCGACCTTC 853
Db 671 GACCGCGGGGCGGGGAGGCGCAACCGTGTCTATTTTGGCTGGGGGCGACCTTC 730
Qy 854 GATGTGTCGGTTCCTCCATTGAACCGCGGTGTCTTTGAGGTGAAGCACTGCTGGAGAT 913
Db 731 GATGTGTCGGTTCCTCCATTGACGCTGTGTCTTTGAGGTGAAGCACTGCTGGAGAT 790
Qy 914 ACCCACTGGGAGGAGGACTTTCACAAACCGGCTCGTGAACCACTTCATGGNAGNATTC 973
Db 791 ACCCACTGGGAGGAGGACTTTCACAAACCGGCTCGTGAACCACTTCATGGNAGNATTC 850
Qy 974 CGCGGGAAGCATGGGAAGGACCTGAGCGGGAACAAAGCGTGCCTGCGCAGGCTGCGCACA 1033
Db 851 CGCGGGAAGCATGGGAAGGACCTGAGCGGGAACAAAGCGTGCCTGCGCAGGCTGCGCACA 910
Qy 1034 GCCTGTGAGCGCGCAAGCGCAACCCGCTCTCCAGCACCCAGGCGACCTCGAGATAGAC 1093
Db 911 GCCTGTGAGCGCGCAAGCGCAACCCGCTCTCCAGCACCCAGGCGACCTCGAGATAGAC 970
Qy 1094 TCCCTGTTGAGGGCGTGGACTTCTACAAGTCCATCACTGCTGCCGCTTTGAGGAATG 1153
Db 971 TCCCTGTTGAGGGCGTGGACTTCTACAAGTCCATCACTGCTGCCGCTTTGAGGAATG 1030
Qy 1154 TGCTCAGACCTCTTCGCGACACCTCGAGCGGCTGGGAAGAGGCGCTCGGGATGCCAAG 1213
Db 1031 TGCTCAGACCTCTTCGCGACACCTCGAGCGGCTGGGAAGAGGCGCTCGGGATGCCAAG 1090
Qy 1214 TTGGAACAAGGCCAGATTCATGACTTGTCTGCGGGGAGGGCTCCATCGCATCCCCAA 1273
Db 1091 TTGGAACAAGGCCAGATTCATGACTGCTCTCTGTGGG-GGGCTCCACTCGCATCCCCAA 1149
Qy 1274 GGTGAGAGTTGTCGAGGACTTCTCAACGGCAAGGCTGACAGAGCATCAACCC 1333
Db 1150 GGTGAGAGTTGTCGAGGACTTCTCAACGGCAAGGCTGACAGAGCATCAACCC 1209
Qy 1334 TGATCAGGCTGTGGCTTATGGGTGTGCTGTGAGCGCGCGCTGTTGTATGGGGGACAAATG 1393

Db 1210 TGATGAGGCTGTGGCTATGGGCTGCTGTGTCAGGGCGCGTGTGATGGGGACAAATG 1269
Qy 1394 TGAGAAAGTGCAGGATCTCTGCTGCTGATGTGGCTCCCTCTGCTCTGCGGCTGGAGAC 1453
Db 1270 TGAGAAAGTGCAGGATCTCTGCTGCTGATGTGGCTCCCTCTGCTCTGCGGCTGGAGAC 1329
Qy 1454 AGCAGGTGGGCTGATGATCACCACGCTGATCCAGAGGAACGCACTATCCCAACCAAGCAGAC 1513
Db 1330 AGCAGGTGGGCTGATGATCACCACGCTGATCCAGAGGAACGCACTATCCCAACCAAGCAGAC 1389
Qy 1514 CCAGACTTTTACCACCTACTCGGACAAACGACCTGGGGTCTTCATCCAGGTGTATGAGG 1572
Db 1390 CCAGACTTTTACCACCTACTCGGACAAACGACCTGGGGTCTTCATCCAGGTGTATGAGG 1448
RESULT 3
AAF18262
ID AAF18262 standard; DNA; 2361 BP.
XX AAF18262;
XX 14-MAR-2001 (first entry)
XX Lung cancer associated polynucleotide sequence SEQ ID 281.
DB Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardiocactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antinefctive; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease; ds.
XX Homo sapiens.
XX WO200055180-A2.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US005918.
XX 12-MAR-1999; 99US-0124270P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX Ruben SM;
XX WPI; 2000-587514/55.
XX P-PSDB; AAB58386.
XX Lung cancer associated gene sequences, referred to as lung cancer
XX antigens, useful for treatment, prevention, and diagnosis of disorders
XX such as lung cancer.
XX Claim 1; Page 740-741; 1425pp; English.
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
XX associated proteins represented in AAB58106 - AAB58548. Lung cancer
XX associated proteins and polynucleotide sequences, their agonists, and
XX antagonists may have neuroprotective; cytostatic; cardiocactive;
XX immunomodulatory; muscular active general; vulnerary; gastrointestinal
XX general; nephrotropic; antinefctive; gynecological; or antibacterial
XX activity. The invention also includes antibodies specific for the protein
XX or polynucleotide sequences. The lung cancer associated polynucleotide
XX sequences may be used for detection of lung cancer, chromosome
XX identification, as chromosome markers, and for numerous other diagnostic
XX or research purposes. The proteins may be used to treat disorders such as
XX neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
XX cardiovascular, renal, and proliferative disorders. The proteins may also
XX be used in the treatment of wounds and infectious diseases
XX Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
XX used in the course of the invention for the identification and
XX characterisation of the polynucleotide and protein sequences

Qy 692 AACTCGAGCCAGGCCACCAAGACGCGGGGCCATCGCGGGCTCAAGTGTCTCCG 751
Db |||||
Qy 569 GACTCGACGCGCAGGCCACCAAGACGCGGGGCCATCGCGGGCTCAAGTGTCTCCG 628
Db |||||
Qy 752 ATCATCAATGAGGCCACCGCAGCAGCCATCGCTATGGCTTGGACCGCGGGCGCGGGA 811
Db |||||
Qy 629 ATCATCAATGAGGCCACCGCAGCAGCCATCGCTATGGCTTGGACCGCGGGCGCGGGA 688
Db |||||
Qy 812 AAGCGCAAGCTGTCAATTTTGAACCTGGGTGGGGACCTTCGATGTGTCTCTCC 871
Db |||||
Qy 689 GAGCGCAAGCTGTCAATTTTGAACCTGGGTGGGGACCTTCGATGTGTCTCTCC 748
Db |||||
Qy 872 ATTGACGCGGTGTCTTGGGTGAAGCCACTGTGGAGATACCCACTGGAGGAG 931
Db |||||
Qy 749 ATTGACGCGGTGTCTTGGGTGAAGCCACTGTGGAGATACCCACTGGAGGAG 808
Db |||||
Qy 932 GACTTCGACAAACCGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 991
Db |||||
Qy 809 GACTTCGACAAACCGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 868
Db |||||
Qy 992 GACTTCGAGCGGGAACAAGCGTCCCTGCGAGGCTGCGCACAGCTGTGAGGCGCCGGAAG 1051
Db |||||
Qy 869 GACTTCGAGCGGGAACAAGCGTCCCTGCGAGGCTGCGCACAGCTGTGAGGCGCCGGAAG 928
Db |||||
Qy 1052 CGCACCCCGTCTCCAGCACCCAGCCACCTGGAGATAGACTCCCTGTTTCGAGGGCGTG 1111
Db |||||
Qy 929 CGCACCCCGTCTCCAGCACCCAGCCACCTGGAGATAGACTCCCTGTTTCGAGGGCGTG 988
Db |||||
Qy 1112 GACTTCTACAAAGTCCATCACTCGTCCCGCTTTTGAAGAACTGTGCTCAGACCTCTTCCGC 1171
Db |||||
Qy 989 GACTTCTACAGTCCATCACTCGTCCCGCTTTTGAAGAACTGTGCTCAGACCTCTTCCGC 1048
Db |||||
Qy 1172 AGCACCTTGGAGCCGCTGAGAAAGCCCTGCGGATGCCAAGCTGGAACAAGGCCAGATT 1231
Db |||||
Qy 1049 AGCACCTTGGAGCCGCTGAGAAAGCCCTGCGGATGCCAAGCTGGAACAAGGCCAGATT 1108
Db |||||
Qy 1232 CATGACTTCGCTCGGGGGGGGCTCCACTCGCATCCCAAGTGCAGAAAGTGTCTGCA 1291
Db |||||
Qy 1109 CATGACTTCGCTCGGGGGGGG-GGGCTCCACAGCATCCCAAGTGCAGAAAGTGTCTGCA 1167
Db |||||
Qy 1292 GGACTTCTTCAACGGCAAGGAGCTGAACAAGACATCAACCTCGATGAGGCTGTGGCCTA 1351
Db |||||
Qy 1168 GGACTTCTTCAACGGCAAGGAGCTGAACAAGACATCAACCTCGATGAGGCTGTGGCCTA 1227
Db |||||
Qy 1352 TGGGCTGTGTGAGGCGCGCTGTGATGGGGGACAAATGTGAGAAAGTGCAGGATCT 1411
Db |||||
Qy 1228 TGGGCTGTGTGAGGCGCGCTGTGATGGGGGACAAATGTGAGAAAGTGCAGGATCT 1287
Db |||||
Qy 1412 CCTGCTGTGGATGTGGCTCCCTCTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGAC 1471
Db |||||
Qy 1288 CCTGCTGTGGATGTGGCTCCCTCTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGAC 1347
Db |||||
Qy 1472 CACGCTGTATCCAGAGGAACGCGCACTATCCCAACCAAGCAGACCCAGACTTTTCAACACCTA 1531
Db |||||
Qy 1348 CACGCTGTATCCAGAGGAACGCGCACTATCCCAACCAAGCAGACCCAGACTTTTCAACACCTA 1407
Db |||||
Qy 1532 CTCGAGCAACAGCTGGGCTTTCATTCAGGTGTATGAGG 1572
Db |||||
Qy 1408 CTCGAGCAACAGCTGGGCTTTCATTCAGGTGTATGAGG 1448
Db |||||

RESULT 5

ABX62981
ID ABX62981 standard; cDNA; 2962 BP.
XX
AC ABX62981;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human activated T cell cDNA #97.
XX
KW T cell; gene; ss; differential expression; T cell activation;
KW antiallergic; cytostatic; immunosuppressive; antimicrobial; gene therapy;

KW allergy; cancer; graft versus host disease; infection;
KW autoimmune disorder.
XX
OS Homo sapiens.
XX
PN US2002137077-A1.
XX
PD 26-SEP-2002.
XX
PF 25-OCT-2001; 2001US-00002600.
XX
PR 25-OCT-2000; 2000US-0243521P.
XX
PA (HOPK/) HOPKINS C M.
PA (PETE/) PETERSON D P.
PA (COCK/) COCKS B G.
PA (HAWK/) HAWKINS P R.
PI Hopkins CM, Peterson DP, Cocks BG, Hawkins PR;
XX
XX WPI; 2003-102381/09.
XX
PT New combination comprising several cDNAs that are differentially
PT expressed in activated T cells, useful for diagnosing, treating, staging
PT or monitoring treatment for allergy, cancer, infectious and/or autoimmune
PT disorders.
XX
PS Claim 1; Page; 180pp; English.
XX
CC This invention relates to the sequences of several cDNAs that are
CC differentially expressed in activated T cells. The sequences of the
CC invention may have antiallergic, cytostatic, immunosuppressive and
CC antimicrobial activity and may be used in gene therapy. The invention
CC also comprises a method for screening samples for differentially
CC expressed genes and a method for detecting these cDNAs by hybridisation.
CC The methods and compositions of the present invention are useful for
CC diagnosing, treating, staging or monitoring treatment for allergy,
CC cancer, chronic graft versus host disease, infectious and/or autoimmune
CC disorders. The present sequence represents a cDNA of the invention that
CC is differentially expressed in activated T cells
XX
SQ Sequence 2962 BP; 643 A; 837 C; 909 G; 573 T; 0 U; 0 Other;
Query Match 17.3%; Score 431; DB 8; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3.3e-198;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 198 CCGTGGCTTCAGCATCCGACAAAGCTTCAGCCATGCGAGCCCGGAGCTCGCGG 257
Db |||||
Qy 699 CCGTGGCTTCAGCATCCGACAAAGCTTCAGCCATGCGAGCCCGGAGCTCGCGG 758
Db |||||
Qy 258 TGGGCATCGACTGGGCACCACTTACTCGTGTGGGGTGTTCAGAGGGCGCGTGG 317
Db |||||
Qy 759 TGGGCATCGACTGGGCACCACTTACTCGTGTGGGGTGTTCAGAGGGCGCGTGG 818
Db |||||
Qy 318 AGATCTCTGGCAACGACGAGGGCAACCGCACCGCCAGAGCGGCCCTTCAACCGACA 377
Db |||||
Qy 819 AGATCTCTGGCAACGACGAGGGCAACCGCACCGCCAGAGCTAGTGGCTTCAACCGACA 878
Db |||||
Qy 378 CCGAGCGGCTGGTGGGGGACCGCGCCAAAGAGAGCGGGCGCCCTGAACCCCGACACCG 437
Db |||||
Qy 879 CCGAGCGGCTGGTGGGGGACCGCGCCAAAGAGAGCGGGCGCCCTGAACCCCGACACCG 938
Db |||||
Qy 438 TGTTCGATGCAAGCGGCTGATTCGGGGCGCAAGTTCGCGGACACACCGTGCAGTCCGACA 497
Db |||||
Qy 939 TGTTCGATGCAAGCGGCTGATTCGGGGCGCAAGTTCGCGGACACACCGTGCAGTCCGACA 998
Db |||||
Qy 498 TGAAGCACTGGCCCTTCAGGTGTGAGCGAGGGCGGCAAGCTGCGGTATGCT 557
Db |||||
Qy 999 TGAAGCACTGGCCCTTCGGGTGTGAGCGAGGGCGGCAAGCTGCGGTATGCT 1058
Db |||||
Qy 558 ACCGCGGGGAGCAAGACGTTCTTACCCGAGGAGATCTCGTCCATGCTGTGAGCAAGA 617
Db |||||

```
Db 1059 ACCGCGGGAGGACAAAGACGTTTACCCCGAGGAGATCTCGTCCATGCTGAGCAAGA 1118
Qy 618 TGAAGGAGACGGCGGCGGTACTCTGGGCGAGCCCGTGAAGCAGCAGTGTATCACCGTGC 677
Db 1119 TGAAGGAGACGGCGGCGGTACTCTGGGCGAGCCCGTGAAGCAGCAGTGTATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180

RESULT 6
ADI61704
ID ADI61704 standard; cDNA; 2962 BP.
XX
AC ADI61704;
DT 16-DEC-2004 (first entry)
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 349676.8.
XX
KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
KW brain disorder.
XX
OS Homo sapiens.
XX
PN US6682888-B1.
XX
PD 27-JAN-2004.
XX
PF 05-MAY-2000; 2000US-00566921.
XX
PR 05-MAY-2000; 2000US-00566921.
XX
PA (INCY-) INCYTE CORP.
XX
PI Loring JF, Tingley DW, Edwards CM;
XX
DR WPI; 2004-118572/12.
XX
DE New composition comprising cDNAs that are differentially expressed in
PT brain disorders, useful for diagnosing or treating Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 72; 223pp; English.
XX
CC The invention relates to a new composition comprising ADI61633-
CC ADI61704 and their complements that are cDNAs differentially expressed in
CC brain disorders. Also included are a high throughput method for detecting
CC differential expression of one or more cDNAs in a sample containing
CC nucleic acids and a high throughput method for screening a library of
CC molecules or compounds to identify a ligand that specifically binds a
CC cDNA. The expression of the each of the cDNAs is downregulated at least
CC two-fold in the brain of the subjects with Alzheimer's disease (ADI61633-
CC ADI61727) or upregulated at least two fold in Alzheimer's disease
CC (ADI61728-ADI6170). The composition is useful for diagnosing or treating
CC Alzheimer's disease. The present sequence is a cDNA downregulated at
CC least two-fold in the brain of the subjects with Alzheimer's disease.
XX
SQ Sequence 2962 BP; 641 A; 838 C; 909 G; 574 T; 0 U; 0 Other;

Query Match 17.3%; Score 431; DB 13; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3.3e-198;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 198 CGGTGCTCCAGCATCCGACAGAGCTTCAGCCATGAGGCCCCACGGGAGCTCGCGG 257
Db 699 CGGTGCTCCAGCATCCGACAGAGCTTCAGCCATGAGGCCCCACGGGAGCTCGCGG 758
Qy 258 TGGGATCGACCTGGGACACCACTACTCTGTGTGGCGGTGTTTCAGCAGGCGCGGTGG 317
Db 759 TGGGATCGACCTGGGACACCACTACTCTGTGTGGCGGTGTTTCAGCAGGCGCGGTGG 818
Qy 318 AGATCTGGCCAAACGACGAGGGCAACCGCACCGCCAGCTACGTGGCGCTTTCACCGACA 377
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Db 819 AGATCTGGCCAAACGACGAGGCAACCGCACCGCCAGCTACGTGGCGCTTTCACCGACA 878
Qy 378 CCGAGCGGTGTGTCGGGAGCGGGCCCAAGAGCAGCGGCGCTTGAACCCCCCAACAACCG 437
Db 879 CCGAGCGGTGTGTCGGGAGCGGGCCCAAGAGCAGCGGCGCTTGAACCCCCCAACAACCG 938
Qy 438 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTTCGCGGACACACCGGTGCGAGTCCGACA 497
Db 939 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTTCGCGGACACACCGGTGCGAGTCCGACA 998
Qy 498 TGAAGCACTGGCCCTTCCAGGTGTTGAGCGAGGCGGCAAGCCCAAGGTGCGCGTATGCT 557
Db 999 TGAAGCACTGGCCCTTCCAGGTGTTGAGCGAGGCGGCAAGCCCAAGGTGCGCGTATGCT 1058
Qy 558 ACCGCGGGAGGACAAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGCTGAGCAAGA 617
Db 1059 ACCGCGGGAGGACAAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGCTGAGCAAGA 1118
Qy 618 TGAAGGAGACGGCGGCGGTACTCTGGGCGAGCCCGTGAAGCAGCAGTGTATCACCGTGC 677
Db 1119 TGAAGGAGACGGCGGCGGTACTCTGGGCGAGCCCGTGAAGCAGCAGTGTATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180

RESULT 7
AEA43869
ID AEA43869 standard; cDNA; 2962 BP.
XX
AC AEA43869;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human cDNA differentially expressed in brain tissue SEQ ID NO:72.
XX
KW diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
KW muscular-gen.; cytosolic; neuroleptic; nootropic; antidepressant;
KW anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
KW immunotherapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN US2005130171-A1.
XX
PD 16-JUN-2005.
XX
PF 26-JAN-2004; 2004US-00765700.
XX
PR 05-MAY-2000; 2000US-00566921.
XX
PA (INCY-) INCYTE CORP.
XX
PI Loring JF, Tingley DW, Edwards CM;
XX
DR WPI; 2005-456990/46.
XX
CC Composition useful for diagnosis, staging, treating or monitoring
CC treatment of a subject with a brain disorder, comprises several cDNAs
CC that are differentially expressed in brain disorders.
XX
PS Claim 1; SEQ ID NO 72; 231pp; English.
XX
CC The invention relates to a composition (I) for the diagnosis, staging,
CC treatment or for the monitoring of treatment of a subject with a brain
CC disorder. (I) comprises several cDNAs that are differentially expressed
CC in brain disorders and chosen from any one of 138 nucleotide sequences of
CC AEA43798-AEA43935, or their complements. Also described: (1) a high
CC throughput method for detecting differential expression of one or more
CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II)
CC selected from AEA43812, AEA43813, AEA43830, AEA43831, AEA43855, AEA43856,
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CC AEA43983 and AEA43923; (3) an expression vector (III) containing (II);
CC (4) a host cell (IV) containing (III); (5) a protein (V) produced using
CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful
CC for a high throughput method of screening a library of molecules or
CC compounds to identify a ligand which specifically binds a cDNA, where the
CC method involves combining (I) with the library of molecules or compound
CC under conditions to allow specific binding and detecting specific binding
CC between each cDNA and a molecule or compound. (IV) is useful for
CC producing a protein, which involves culturing (IV) under conditions for
CC the expression of the protein and recovering the protein from the
CC culture. (V) is useful for high throughput method for screening a library
CC of molecules or compounds to identify a ligand which specifically binds
CC (V), where the method involves combining (V) or its portion with the
CC library of molecules or compound under conditions to allow specific
CC binding and detecting specific binding between (V) and a molecule or
CC compound. (V) is useful for purifying a ligand from a sample, which
CC involves combining (V) or its portion with the sample under conditions to
CC allow specific binding, recovering the bound protein and separating the
CC protein from ligand. (V) is also useful for producing an antibody which
CC involves immunizing an animal with (V) or its portion under conditions to
CC elicit an antibody response, isolating animal antibodies and screening
CC the isolated antibodies with the protein. (II) is useful in gene therapy
CC for the treatment or prevention of conditions and disorders associated
CC with immune response. The present sequence represents a human cDNA
CC sequence which is differentially expressed in brain tissues, which is
CC used in the exemplification of the present invention.

XX SQ Sequence 2962 BP; 641 A; 838 C; 909 G; 574 T; 0 U; 0 Other;

Query Match 17.3%; Score 431; DB 14; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3.3e-198;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 198 CCGTGGCTCCAGCATCCGACAAAGAGCTTCAGCCATCAGGCCCCACCGAGCTCGCG 257
Db 699 CCGTGGCTCCAGCATCCGACAAAGAGCTTCAGCCATCAGGCCCCACCGAGCTCGCG 758
Qy 258 TGGGATCGACTGGGCAACCACTACTCTGTGGTGGGGGTGTTTCAGCAGGGCCGCGTGG 317
Db 759 TGGGATCGACTGGGCAACCACTACTCTGTGGTGGGGGTGTTTCAGCAGGGCCGCGTGG 818
Qy 318 AGATCCTGGCCAAACGACGAGGCAACCGCACGCCCGAGCTACGTGGCCCTTACCGACA 377
Db 819 AGATCCTGGCCAAACGACGAGGCAACCGCACGCCCGAGCTACGTGGCCCTTACCGACA 878
Qy 378 CCGAGCGCTGTGTGGGGAACGGCCAAAGAGCAGCGGCGCCCTGAACCCCCACACACCG 437
Db 879 CCGAGCGCTGTGTGGGGAACGGCCAAAGAGCAGCGGCGCCCTGAACCCCCACACACCG 938
Qy 438 TGTTCGATGCCAGCGGCTGATCGGGCCCAAGTTCCGGACACACGTCAGTCGGACA 497
Db 939 TGTTCGATGCCAGCGGCTGATCGGGCCCAAGTTCCGGACACACGTCAGTCGGACA 998
Qy 498 TGAACACTGGCCCTTCCAGGTGGTGGAGCGGGGGGCAAGCCCAAGTGGCGGTATGCT 557
Db 999 TGAACACTGGCCCTTCCAGGTGGTGGAGCGGGGGGCAAGCCCAAGTGGCGGTATGCT 1058
Qy 558 ACCCGGGGAGGACAAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGTGTGTGACGAAGA 617
Db 1059 ACCCGGGGAGGACAAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGTGTGTGACGAAGA 1118
Qy 618 TGAAGGACGCGCCAGCGTACTTGGGCGAGCCCGTAGCAGCCAGTCATCACCGTGC 677
Db 1119 TGAAGGACGCGCCAGCGTACTTGGGCGAGCCCGTAGCAGCCAGTCATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180

RESULT 8
ADP66225/c
ID ADP66225 standard; cDNA; 531 BP.

XX AC ADP66225;
XX DT 26-AUG-2004 (first entry)
XX DE Human cDNA from gene modulated by pro-inflammatory cytokines #45.
XX KW Human; ss; cytokine; peripheral blood mononuclear cell; PBMC;
KW differential expression; immune disorder; pro-inflammatory disorder;
KW viral infection; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; multiple sclerosis;
KW encephalomyelitis; inflammatory bowel disease; psoriasis;
KW pemphigus vulgaris; anti-inflammatory disorder; bacterial infection;
KW parasitic infection; allergy; topic disorder;
KW chronic graft-versus-host disease; scleroderma;
KW systemic lupus erythematosus; probe.
XX OS Homo sapiens.
XX PN US2004110194-A1.
XX PD 10-JUN-2004.
XX PF 07-AUG-2003; 2003US-00637855.
XX PR 05-NOV-1999; 99US-00435247.
XX PA (INCY-) INCYTE CORP.
XX PI Sornasse T, Cocks BG, Sanjawala B;
XX WPI; 2004-486580/46.
XX PT A composition comprises polynucleotides that are modulated in response to
XX PT cytokines, useful for diagnosing or treating conditions associated with
XX PT an immune response, e.g. infection, diabetes, allergies or scleroderma.
XX PS Claim 1; SEQ ID NO 217; 210pp; English.
XX CC The invention relates to a composition comprising polynucleotides whose
XX CC expression is modulated by cytokines, where the polynucleotides comprise
XX CC any of the cDNA fragments (isolated from peripheral blood mononuclear
XX CC cells (PBMC)) and appearing as ADP66009-ADP66524, or their complements.
XX CC Also included are a substantially purified polynucleotide whose
XX CC expression is modulated by cytokines comprising at least a fragment of a
XX CC gene selected from ADP66009-ADP66251, a high throughput method for
XX CC detecting a polynucleotide in a sample, methods of purifying ligands, an
XX CC expression vector containing the above polynucleotide, a host cell
XX CC containing the expression vector, a method for producing a protein, a
XX CC protein or its portion produced by the method, high throughput methods of
XX CC screening a library of molecules or compounds to identify a ligand or at
XX CC least one ligand which specifically binds a protein, and a method of
XX CC screening a sample from a patient for an immune response, disorder,
XX CC condition or disease. The immune disorder, condition or disease is a pro-
XX CC inflammatory disorder (selected from viral infections, rheumatoid
XX CC arthritis, insulin-dependent diabetes mellitus, multiple sclerosis,
XX CC encephalomyelitis, inflammatory bowel disease, psoriasis, and pemphigus
XX CC vulgaris) and an anti-inflammatory disorder (selected from bacterial and
XX CC parasitic infections, allergies and other topic disorders, chronic graft-
XX CC versus-host disease, scleroderma and systemic lupus erythematosus). The
XX CC composition and methods are useful for detecting genes modulated in
XX CC response to human cytokines or for diagnosing useful for diagnosing or
XX CC treating conditions associated with an immune response. The present
XX CC sequence is a cDNA fragment from a gene whose expression is modulated by
XX CC pro-inflammatory cytokines. NOTE: Details of the expression levels of the
XX CC genes in response to various cytokines are said to be contained in tables
XX CC 1-4, but these tables are not included in the specification.
XX SQ Sequence 531 BP; 151 A; 141 C; 118 G; 121 T; 0 U; 0 Other;

Query Match 17.2%; Score 429; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 3e-197;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2024	GGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGGCGCTGCTGCC	2083
Db	429	GGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGGCGCTGCTGCC	370
Qy	2084	TGGGGGCGAGCAGTTGTGTAGCGCTCAAGCCCAACAGGGGAGCCCCAGCACCGGCCCCCATCAT	2143
Db	369	TGGGGGCGAGCAGTTGTGTAGCGCTCAAGCCCAACAGGGGAGCCCCAGCACCGGCCCCCATCAT	310
Qy	2144	TGAGGAGGTTGATTTGAATGGGCCCTTCGTGTAAGTCAGCTGTGACTCTCAGGGCGTATGCT	2203
Db	309	TGAGGAGGTTGATTTGAATGGGCCCTTCGTGTAAGTCAGCTGTGACTCTCAGGGCGTATGCT	250
Qy	2204	ATGGGCGCTTCPAGACTGCTCTTATGATCTCTGCCCTTCAGAGATGAAGGGCTTGGGGGGG	2263
Db	249	ATGGGCGCTTCPAGACTGCTCTTATGATCTCTGCCCTTCAGAGATGAAGGGCTTGGGGGGG	190
Qy	2264	TCCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGTCCTTTTCAGCTTTTGGG	2323
Db	189	TCCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGTCCTTTTTCAGCTTTTGGG	130
Qy	2324	GGGAGGGCGGTTCACTCTCTCTCTCAATAAAAAAGTCATTAATTTATTTAAAACTTGT	2383
Db	129	GGGAGGGCGGTTCACTCTCTCTCTCAATAAAAAAGTCATTAATTTATTTAAAACTTGT	70
Qy	2384	GTGGCATTCTAAACATTCGTTTCACCTATATTTGTGTATTTTGTACTCTGTATGTATGAA	2443
Db	69	GTGGCATTCTAAACATTCGTTTCACCTATATTTGTGTATTTTGTACTCTGTATGTATGAA	10
Qy	2444	TTTTGTATTAT	2452
Db	9	TTTTGTATTAT	1

RESULT 9

ABL68660	
ID	ABL68660 standard; DNA; 2492 BP.
XX	
XX	
AC	ABL68660;
XX	
XX	
DT	15-MAY-2002 (first entry)
DE	
DE	Kidney cancer related gene sequence SEQ ID NO:6997.
XX	
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.

PR	05-JUN-2000;	2000US-020473P.
PR	15-JUN-2000;	2000US-0209531P.
PR	18-SEP-2000;	2000US-0233133P.
PR	10-SEP-2000;	2000US-0233617P.
PR	20-SEP-2000;	2000US-0234009P.
PR	20-SEP-2000;	2000US-0234034P.
PR	20-SEP-2000;	2000US-0234052P.
PR	22-SEP-2000;	2000US-0234509P.
PR	22-SEP-2000;	2000US-0234567P.
PR	23-SEP-2000;	2000US-0234523P.
PR	25-SEP-2000;	2000US-0234924P.
PR	25-SEP-2000;	2000US-0235077P.
PR	25-SEP-2000;	2000US-0235082P.
PR	25-SEP-2000;	2000US-0235134P.
PR	25-SEP-2000;	2000US-0235280P.
PR	26-SEP-2000;	2000US-0235637P.

PR	26-SEP-2000; 2000US-0235638P.
PR	27-SEP-2000; 2000US-0235711P.
PR	27-SEP-2000; 2000US-0235720P.
PR	27-SEP-2000; 2000US-0235840P.
PR	27-SEP-2000; 2000US-0235863P.
PR	28-SEP-2000; 2000US-0236028P.
PR	28-SEP-2000; 2000US-0236032P.
PR	28-SEP-2000; 2000US-0236033P.
PR	28-SEP-2000; 2000US-0236034P.
PR	28-SEP-2000; 2000US-0236109P.
PR	28-SEP-2000; 2000US-0236111P.
PR	29-SEP-2000; 2000US-0236842P.
PR	29-SEP-2000; 2000US-0236891P.
PR	02-OCT-2000; 2000US-0237172P.
PR	02-OCT-2000; 2000US-0237173P.
PR	02-OCT-2000; 2000US-0237278P.
PR	02-OCT-2000; 2000US-0237294P.
PR	02-OCT-2000; 2000US-0237295P.
PR	02-OCT-2000; 2000US-0237316P.
PR	03-OCT-2000; 2000US-0237425P.
PR	03-OCT-2000; 2000US-0237598P.
PR	03-OCT-2000; 2000US-0237604P.
PR	03-OCT-2000; 2000US-0237606P.
PR	03-OCT-2000; 2000US-0237608P.
PR	01-NOV-2000; 2000US-0244867P.
PR	01-NOV-2000; 2000US-0245084P.
XX	
PA	(AVAL-) AVALON PHARM.
XX	
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
FI	Soppet DR, Weaver Z;
XX	
DR	WPI; 2002-188264/24.
XX	
PT	Screening for anti-neoplastic agent involves exposing cells to a chemical
PT	agent to be tested for anti-neoplastic activity, and determining a change
PT	in expression of a gene of a signature gene set.
XX	
PS	Claim 1; SEQ ID NO 6997; 44pp; English.
XX	
CC	The present invention describes a method (M1) for screening for an anti-
CC	neoplastic agent. The method involves exposing cells to a chemical agent
CC	to be tested for anti-neoplastic activity, determining a change in
CC	expression of at least one gene (I) of a signature gene set, where (I)
CC	comprises a sequence (S) selected from 8447 sequences (given in ABLE1664
CC	to ABU70110), or is at least 95% identical to (S), where a change in
CC	expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC	activity and can be used in gene therapy. M1 can be used for screening an
CC	anti-neoplastic agent, and can be used for producing a product which is
CC	the data collected with respect to the anti-neoplastic agent as a result
CC	of M1, and the data is sufficient to convey the chemical structure and/or
CC	properties of the agent. M1 can be used in the treatment of cancer such
CC	as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC	prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC	cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC	cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC	tumour
XX	
SQ	Sequence 2492 BP; 553 A; 693 C; 790 G; 466 T; 0 U; 0 Other;
Query Match	13.2%; Score 329; DB 6; Length 2492;
Best Local Similarity	100.0%; Pred.No. 1.le-148;
Matches 329; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Qy	187 GGCGAGAGCCTTCGTGGCTTCCAGCATCCGACAGAAGACTTCAGGCATCGAGGCCCCACG 246
Dd	205 GGCGAGAGCCTTCGTGGCTTCCAGCATCCGACAGAAGACTTCAGGCATCGAGGCCCCACG 264
Qy	247 GGAGCTCGCGTGCGGATCCGACCTGGCGCACCACTACTCGNGCGTGGCGGTTCACGA 306
Dd	265 GGAGCTCGCGTGCGGATCCGACCTGGCGCACCACTACTCGNGCGTGGCGGTTCACGA 324
Qy	307 GGGCCGCGTGAGAGATCTTGGCCAAACGACCGAGGGCAAACGACACCGCCAGCTACGTGGCG 366

```
Db 325 GGGCGCGTGGAGATCTTGGCCACAGACACGGGACACCGACCGCCAGCTAGTGGC 384
Qy 367 CTTACCGACACCGAGCGGCTGGTGGGGACCGCGCCAAAGACCGAGCGGCCCTGAACCC 426
Db 385 CTTACCGACACCGAGCGGCTGGTGGGGACCGCGCCAAAGACCGAGCGGCCCTGAACCC 444
Qy 427 CCACACACCGTGTTCGATGTCACACCGGCTGATCGGGGCGCAAGTTCGGGACACACCGGT 486
Db 445 CCACACACCGTGTTCGATGTCACACCGGCTGATCGGGGCGCAAGTTCGGGACACACCGGT 504
Qy 487 CGAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 CGAGTCGGACATGAAGCACTGGCCCTTCC 533
```

RESULT 10

ABK84553

ID ABK84553 standard; cDNA; 2492 BP.

XX AC ABK84553;

XX DT 14-AUG-2002 (first entry)

XX DE Human cDNA differentially expressed in granulocytic cells #1124.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.

XX OS Homo sapiens.

XX PN WO200228999-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX PS WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.

XX Claim 1; SEQ ID NO 1124; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2492 BP; 553 A; 683 C; 790 G; 466 T; 0 U; 0 Other;

Query Match 13.2%; Score 329; DB 6; Length 2492;

Best Local Similarity 100.0%; Pred. No. 1.1e-148;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCTCCAGCATCCGACAAAGAAGCTTCAGCCATGAGGCCCCACG 246
Db 205 GGCAGCAGCCTCCGTGGCCTCCAGCATCCGACAAAGAAGCTTCAGCCATGAGGCCCCACG 264
Qy 247 GGAGCTCGGTGGGCATCGACCTGGGCACACCTACTCTGTCGTGGCGGTGTTTCAGCA 306
Db 265 GGAGCTCGGTGGGCATCGACCTGGGCACACCTACTCTGTCGTGGCGGTGTTTCAGCA 324
Qy 307 GGGCCGCGTGAGAGATCCTGGCCAAACGACGAGGGCAACCGCACCGCCAGCTACGTGGC 366
Db 325 GGGCCGCGTGAGATCCTGGCCAAACGACGAGGGCAACCGCACCGCCAGCTACGTGGC 384
Qy 367 CTTACCGACACCGAGCGGCTGGTGGGGAGCGGGCCAAAGAGCCAGCGGCCCTGAACCC 426
Db 385 CTTACCGACACCGAGCGGCTGGTGGGGAGCGGGCCAAAGAGCCAGCGGCCCTGAACCC 444
Qy 427 CCACACACCGTGTTCGATGTCACACCGGCTGATCGGGCGCAAGTTCGGCGGACACACCGGT 486
Db 445 CCACACACCGTGTTCGATGTCACACCGGCTGATCGGGCGCAAGTTCGGCGGACACACCGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 11

ACA64921

ID ACA64921 standard; DNA; 2492 BP.

XX AC ACA64921;

XX DT 27-JUN-2003 (first entry)

XX DE Human HSP70B DNA corresponding to X51757.

XX Human; chronic inflammatory joint disease; infection; tumour;
KW antiinflammatory; cycostatic; antiarthritic; antirheumatic;
KW immunosuppressive; gene therapy; etiologic pathogenicity; ds.

XX OS Homo sapiens.

XX PN DE10127572-A1.

XX PD 05-DEC-2002.

XX PF 30-MAY-2001; 2001DE-01027572.

XX

Qy 247 GGAGCTCGCGTGGGCATCGACCTGGGTCAGCCACCACTACTCTGCTGGCGGTGTTTCAGCA 306
Dy 265 GGAGCTCGCGTGGGCATCGACCTGGGTCAGCCACCACTACTCTGCTGGCGGTGTTTCAGCA 324
Qy 307 GGGCCGCGTGAGATCTCTGGCCCAACGACGAGGGAACCGCACCAACCGCCAGCTACGTGGC 366
Dy 325 GGGCCGCGTGAGATCTCTGGCCCAACGACGAGGGAACCGCACCAACCGCCAGCTACGTGGC 384
Qy 367 CTTACCCGACACCGAGCGGCTGTGCGGGAACCGGCCCAAGAGCCAGCGGCCCTTGAACCC 426
Dy 385 CTTACCCGACACCGAGCGGCTGTGCGGGAACCGGCCCAAGAGCCAGCGGCCCTTGAACCC 444
Qy 427 CCACAACACCGTTCGATGTCGACGCGCTGATCGGGGCAAGTTCGGGGACACACCGGT 486
Dy 445 CCACAACACCGTTCGATGTCGACGCGCTGATCGGGGCAAGTTCGGGGACACACCGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Dy 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 13

ABA96361

ID ABA96361 standard; DNA; 1932 BP.

XX ABA96361;

AC ABA96361;

XX 21-MAR-2002 (first entry)

XX Human schizophrenia/SCZ associated gene HSP70B SEQ ID NO 1.

DE Human; chromosome 1q22; SCZ; schizophrenia; in utero screening;

XX Human; chromosome 1q22; SCZ; schizophrenia; in utero screening;

KW gene therapy; heat shock protein 70B; HSP70B; gene; ds.

XX Homo sapiens.

OS Homo sapiens.

XX Location/Qualifiers

Key 1..1932

FT CDS /tag= a

FT /product= "SCZ/HSP70B"

XX WO200150412-A1.

XX 29-NOV-2001.

XX 23-APR-2001; 2001WO-US013086.

XX 21-APR-2000; 2000US-0198900P.

XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Brzustowicz LM, Bassett AS;

XX WPI; 2002-083121/11.

XX P-PSDB; AM48711.

XX Diagnosing susceptibility to schizophrenia comprises determining presence

PT of allele of linked polymorphic marker on chromosome 1q22 and linked to

PT variant form of SCZ gene associated with schizophrenia phenotype.

XX Claim 19; Page 69-70; 83pp; English.

XX The invention relates to diagnosing susceptibility to schizophrenia in a

CC patient comprising determining the presence/absence of an allele of a

CC polymorphic marker in the DNA of a patient, where the polymorphic marker

CC is within the chromosome segment 1q22 bordered by D1S2705, D1S1679 and

CC linked to the DNA segment SCZ having a variant form associated with

CC phenotype of schizophrenia, where the allele is in phase with the variant

CC form of SCZ and the presence of the allele indicates susceptibility to

CC schizophrenia. The method can be used for in utero screening of fetuses

CC for the presence of a variant SCZ allele. Identification of such

CC variations offers the possibility of gene therapy and for couples known

CC to be at risk of giving rise to an affected progeny, diagnosis can be

CC combined with in vitro reproduction procedures to identify an embryo

CC having wild-type SCZ alleles before implantation. Screening children

CC shortly after birth allows administration of appropriate treatment at an

CC early stage of detection. The genetic tests provide a highly accurate

CC assay for diagnosing schizophrenia and schizophrenia susceptibility. The

CC SCZ gene encodes a previously isolated sequence encoding human heat shock

CC protein 70B (HSP70B, GenBank Accession Number NM002155)

XX Sequence 1932 BP; 423 A; 552 C; 632 G; 325 T; 0 U; 0 Other;

Qy Query Match 11.4%; Score 283; DB 6; Length 1932;

Dy Best Local Similarity 100.0%; Pred. No. 2.3e-126;

Qy Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 233 ATGAGGCCCCACCGGAGCTCGCGGTGGGATCGACCTGGGCACCACTACTCTGCGGTG 292

Dy 1 ATGAGGCCCCACCGGAGCTCGCGGTGGGATCGACCTGGGCACCACTACTCTGCGGTG 60

Qy 293 GCGGTGTTTCAGCAGGGCCGCGTGGAGATCTCTGCCAACACCAAGGGCAACCCACACG 352

Dy 61 GCGGTGTTTCAGCAGGGCCGCGTGGAGATCTCTGCCAACACCAAGGGCAACCCACACG 120

Qy 353 CCCAGTACGTGGCTTTCACCGACACCGAGCGGTGGTGGGGACCGGCCCAAGCCAG 412

Dy 121 CCCAGTACGTGGCTTTCACCGACACCGAGCGGTGGTGGGGACCGGCCCAAGCCAG 180

Qy 413 GCGGCTCTGAACCCCAACACCGGTGTTGATGCCAAGCGGTGATCGGGCGCAAGTTC 472

Dy 181 GCGGCTCTGAACCCCAACACCGGTGTTGATGCCAAGCGGTGATCGGGCGCAAGTTC 240

Qy 473 GCGGACACCAACCGGTGTCAGTCGACATGACACTGGCCCTTCC 515

Dy 241 GCGGACACCAACCGGTGTCAGTCGACATGACACTGGCCCTTCC 283

RESULT 14

ADD18651

ID ADD18651 standard; DNA; 1932 BP.

XX ADD18651;

XX 15-JAN-2004 (first entry)

XX Human disease related protein DNA sequence SeqID82.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological;

XX antiarteriosclerotic; vulnary; gene therapy;

XX hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;

XX inflammation; erythropoiesis; glycolysis; gluconeogenesis;

XX glucose transportation; catecholamine synthesis; iron transport;

XX nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;

XX retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;

XX inflammatory condition; wound healing; gene; ds.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX P-PSDB; ADD18650.

XX New substantially purified polypeptide, useful for diagnosing or treating

PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX
XX
XX Claim 27; SEQ ID NO 82; 424pp; English.
XX
XX This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transposition, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX
XX
XX Sequence 1932 BP; 423 A; 552 C; 632 G; 325 T; 0 U; 0 Other;

Query Match 11.4%; Score 283; DB 10; Length 1932;
Best Local Similarity 100.0%; Pred. No. 2.3e-126;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 233 ATGCAGGCCCCACGGAGCTCGGGTGGGATCGACCTGGGCACCACTACTCTGTCGGTG 292
DB 1 ATGCAGGCCCCACGGAGCTCGGGTGGGATCGACCTGGGCACCACTACTCTGTCGGTG 60
QY 293 GCGGTGTTTCAGCAGGGCCGCGTGGAGATCCTGGCCAAACGACGAGGCAACGCCACG 352
DB 61 GCGGTGTTTCAGCAGGGCCGCGTGGAGATCCTGGCCAAACGACGAGGCAACGCCACG 120
QY 353 CCCAGCTACGTGGCCCTTACCCGACACCGAGCGGCTGGTGGGACCGGGCCAAAGGCCAG 412
DB 121 CCCAGCTACGTGGCCCTTACCCGACACCGAGCGGCTGGTGGGACCGGGCCAAAGGCCAG 180
QY 413 GCGGCTGTGTAACCCCAACACCGCTGTTTCGATGCCAAGCGGCTGATCGGGGCAAGTTTC 472
DB 181 GCGGCTGTGTAACCCCAACACCGCTGTTTCGATGCCAAGCGGCTGATCGGGGCAAGTTTC 240
QY 473 GCGGACACCAACCGTGCAGTGGGACATGAAGCACTGGCCCTTCC 515
DB 241 GCGGACACCAACCGTGCAGTGGGACATGAAGCACTGGCCCTTCC 283

RESULT 15

ADP12821
ID ADP12821 standard; DNA; 1932 BP.
XX
XX AC
XX ADP12821;
XX
XX 12-AUG-2004 (first entry)
XX
XX DE Reference mRNA sequence #35.
XX
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2004042346-A2.
XX
XX PD 21-MAY-2004.
XX
XX PF 24-APR-2003; 2003WO-US012946.
XX
XX PR 24-APR-2002; 2002US-00131831.
XX
XX PR 20-DEC-2002; 2002US-00325899.
XX
XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 65; SEQ ID NO 2830; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprising detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC reference mRNA sequence of the invention which show altered expression in
CC renal transplantation and expression.
XX
XX
XX Sequence 1932 BP; 423 A; 552 C; 632 G; 325 T; 0 U; 0 Other;
SQ
Query Match 11.4%; Score 283; DB 12; Length 1932;
Best Local Similarity 100.0%; Pred. No. 2.3e-126;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 233 ATGCAGGCCCCACGGAGCTCGGGTGGGATCGACCTGGGCACCACTACTCTGTCGGTG 292
DB 1 ATGCAGGCCCCACGGAGCTCGGGTGGGATCGACCTGGGCACCACTACTCTGTCGGTG 60
QY 293 GCGGTGTTTCAGCAGGGCCGCGTGGAGATCCTGGCCAAACGACGAGGCAACGCCACG 352
DB 61 GCGGTGTTTCAGCAGGGCCGCGTGGAGATCCTGGCCAAACGACGAGGCAACGCCACG 120
QY 353 CCCAGCTACGTGGCCCTTACCCGACACCGAGCGGCTGGTGGGACCGGGCCAAAGGCCAG 412
DB 121 CCCAGCTACGTGGCCCTTACCCGACACCGAGCGGCTGGTGGGACCGGGCCAAAGGCCAG 180
QY 413 GCGGCTGTGTAACCCCAACACCGCTGTTTCGATGCCAAGCGGCTGATCGGGGCAAGTTTC 472
DB 181 GCGGCTGTGTAACCCCAACACCGCTGTTTCGATGCCAAGCGGCTGATCGGGGCAAGTTTC 240
QY 473 GCGGACACCAACCGTGCAGTGGGACATGAAGCACTGGCCCTTCC 515
DB 241 GCGGACACCAACCGTGCAGTGGGACATGAAGCACTGGCCCTTCC 283

Search completed: November 3, 2006, 20:46:11
Job time : 1463.41 secs

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Qy 452 CGCGTGATCGGCGCAAGTTCCGCGAACAACACGTCAGTCGAGCATGAAGACATCGGCC 511
Db 329 CGCGTGATCGGCGCAAGTTCCGCGAACAACACGTCAGTCGAGCATGAAGACATCGGCC 388
Qy 512 TTCAGGTGGTGAGCGGGCGCAAGCCCAAGTGGCGATATGCTACCGGGGAGGAC 571
Db 389 TTCGGGTGGTGAGCGGGCGCAAGCCCAAGTGGCGATATGCTACCGGGGAGGAC 448
Qy 572 AAGAGCTTTCTACCCGAGGAGATCTCGTCCATGTGTGCTGAGCAAGATGAAGAGACGGCC 631
Db 449 AAGAGCTTTCTACCCGAGGAGATCTCGTCCATGTGTGCTGAGCAAGATGAAGAGACGGCC 508
Qy 632 GAGCGTACCTGGCGACCGCGTGAAGACACGAGTGATCACCGTGCCCACTATTTCAGT 691
Db 509 GAGCGTACCTGGCGACCGCGTGAAGACACGAGTGATCACCGTGCCCACTATTTCAGT 568
Qy 692 AACTCGAGCGCAGGCCACCAAGGACGCGGGGCTCATCGGGGCTCAAGTGTCTGCCG 751
Db 569 GACTCGAGCGCAGGCCACCAAGGACGCGGGGCTCATCGGGGCTCAAGTGTCTGCCG 628
Qy 752 ATCATCAATGAGGCCACGAGCAGCCATCGCTATGGGCTGGACCGCGGGCGCGGGA 811
Db 629 ATCATCAATGAGGCCACGAGCAGCCATCGCTATGGGCTGGACCGCGGGCGCGGGA 688
Qy 812 AAGCGCAACGTGCTCATTTTGAACCTGGGTGGGGCACCTTCGATGTGTCTCTCC 871
Db 689 GAGCGCAACGTGCTCATTTTGAACCTGGGTGGGGCACCTTCGATGTGTCTCTCC 748
Qy 872 ATTGAGCGCGGTGCTTTGAGGTGAAGCACTGCTGAGATACCCACTCGGAGGAG 931
Db 749 ATTGAGCGCGGTGCTTTGAGGTGAAGCACTGCTGAGATACCCACTCGGAGGAG 808
Qy 932 GACTTCGACAACCGGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 991
Db 809 GACTTCGACAACCGGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 868
Qy 992 GACTGAGCGGGAACAAGCGTGCCCTGCGAGGCTGCGCACAGCTGTGAGCGGCCAAG 1051
Db 869 GACTGAGCGGGAACAAGCGTGCCCTGCGAGGCTGCGCACAGCTGTGAGCGGCCAAG 928
Qy 1052 CGCACCCGCTCTCCAGCACCCAGGCCACCTGGAGATAGACTCCCTGTTCGAGGGGTG 1111
Db 929 CGCACCCGCTCTCCAGCACCCAGGCCACCTGGAGATAGACTCCCTGTTCGAGGGGTG 988
Qy 1112 GACTTCTACAAGTCCATCACTGTCGCGCTTTTGAGGAACCTGTGCTCAGACCTCTTCCGC 1171
Db 989 GACTTCTACAAGTCCATCACTGTCGCGCTTTTGAGGAACCTGTGCTCAGACCTCTTCCGC 1048
Qy 1172 AGCACCTTGAGCCGGTGAGAGGCCCTTGCGGATGCGCAAGCTGGACAAGGCCAGATT 1231
Db 1049 AGCACCTTGAGCCGGTGAGAGGCCCTTGCGGATGCGCAAGCTGGACAAGGCCAGATT 1108
Qy 1232 CATGACTTCTGCTCGGGGGGGGCTCCACTCGCATCCCAAGTGGCAGAAAGTTGCTGCA 1291
Db 1109 CATGACTGCTGCTCGTGGTGGG-GGGCTCCACAGCATCCCAAGGTGCAGAAAGTTGCTGCA 1167
Qy 1292 GGACTTCTTCAACGCGCAAGGAGCTGAACAAGAGCATCAACCTGATGAGGCTGTGGCCTA 1351
Db 1168 GGACTTCTTCAACGCGCAAGGAGCTGAACAAGAGCATCAACCTGATGAGGCTGTGGCCTA 1227
Qy 1352 TGGGTGCTGTGTCAGGCGCGCGTGTGATGGGGGACAAATGTGAGAAAGTGCAGGATCT 1411
Db 1228 TGGGTGCTGTGTCAGGCGCGCGTGTGATGGGGGACAAATGTGAGAAAGTGCAGGATCT 1287
Qy 1412 CCGTGTGCTGGATGTGGCTCCCTCTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGAC 1471
Db 1288 CCGTGTGCTGGATGTGGCTCCCTCTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGAC 1347
Qy 1472 CACGCTGATCCAGAGGAACGCCACTATCCCCCAAGCAGACCCAGACTTTTCAACACCTA 1531
Db 1348 CACGCTGATCCAGAGGAACGCCACTATCCCCCAAGCAGACCCAGACTTTTCAACACCTA 1407
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Qy 1532 CTCGCAACAACAGCTGGGCTCTTCATCCAGGTGTATGAG 1572
Db 1408 CTCGCAACAACAGCTGGGCTCTTCATCCAGGTGTATGAG 1448
```

RESULT 2

```
US-09-566-921-72
; Sequence 72, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; FILE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 72
; LENGTH: 2962
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 349676.8
US-09-566-921-72
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Query Match 17.3%; Score 431; DB 3; Length 2962;
Best Local Similarity 99.8%; Pred. No. 2e-202;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 198 CCGTGGCTTCAGATCCGACAAAGATTCAGCCATGCGAGGCCCAACGGAGCTCGCG 257
Db 699 CCGTGGCTTCAGATCCGACAAAGATTCAGCCATGCGAGGCCCAACGGAGCTCGCG 758
Qy 258 TGGGCATCGACCTGGGCAACCACTACTCTGTCGTCGGGCGTGTTCACGAGGGCGCGTGG 317
Db 759 TGGGCATCGACCTGGGCAACCACTACTCTGTCGTCGGGCGTGTTCACGAGGGCGCGTGG 818
Qy 318 AGATCTCTGGCCAAACGACAGGCGCAACCGCACCGCCAGCTACGTGGCCCTTCACCGACA 377
Db 819 AGATCTCTGGCCAAACGACAGGCGCAACCGCACCGCCAGCTACGTGGCCCTTCACCGACA 878
Qy 378 CCGAGCGGCTGTGTCGGGACCGCGCCAAAGAGCAGCGGCGCCCTGAAACCCCAACACCG 437
Db 879 CCGAGCGGCTGTGTCGGGACCGCGCCAAAGAGCAGCGGCGCCCTGAAACCCCAACACCG 938
Qy 438 TGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACCAACGTCAGTCGGACA 497
Db 939 TGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACCAACGTCAGTCGGACA 998
Qy 498 TGAAGACACTGGCCCTTCAGGTGTGAGCGAGGCGCGCAAGCCCAAGGTGCGCGTATGCT 557
Db 999 TGAAGACACTGGCCCTTCAGGTGTGAGCGAGGCGCGCAAGCCCAAGGTGCGCGTATGCT 1058
Qy 558 ACCCGGGGAGGACAAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGTCGTGAGCAAGA 617
Db 1059 ACCCGGGGAGGACAAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGTCGTGAGCAAGA 1118
Qy 618 TGAAGGAGACGGCGAGGCGGTACCTGGGCGCACCGCTGAGACGACGAGTATCACCGTGC 677
Db 1119 TGAAGGAGACGGCGAGGCGGTACCTGGGCGCACCGCTGAGACGACGAGTATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180
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RESULT 3

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US-08-797-358B-2
; Sequence 2, Application US/08797358B
; Patent No. 6268478
```

GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2379 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-797-358B-2

Query Match 13.2%; Score 329; DB 3; Length 2379;
Best Local Similarity 100.0%; Pred. No. 5.1e-152;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 GGCAGCAGCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATCAGGCCCCACG 246
Db 205 GGCAGCAGCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATCAGGCCCCACG 264
QY 247 GGAGCTCGGTGGGATCGACTGGGACACCTACTACTCTGCTGGGCGTGTTCAGCA 306
Db 265 GGAGCTCGGTGGGATCGACTGGGACACCTACTACTCTGCTGGGCGTGTTCAGCA 324
QY 307 GGGCGCGTGGAGATCCTGGCAACAGCAGGGCAACCGCACCGCCAGCTAGTGGC 366
Db 325 GGGCGCGTGGAGATCCTGGCAACAGCAGGGCAACCGCACCGCCAGCTAGTGGC 384
QY 367 TTTCACCGACACCGAGCGCTGCTGGGACCGCGCCAAAGACGAGCGCGCCCTGAACC 426
Db 385 TTTCACCGACACCGAGCGCTGCTGGGACCGCGCCAAAGACGAGCGCGCCCTGAACC 444
QY 427 CCACAAACCGTGTTCAGATGCAAGCGGTGATCGGGCGCAAGTTCGGGACACCAACG 486
Db 445 CCACAAACCGTGTTCAGATGCAAGCGGTGATCGGGCGCAAGTTCGGGACACCAACG 504
QY 487 GCAGTCGGACATGAGACCTGCCCCCTTC 515
Db 505 GCAGTCGGACATGAGACCTGCCCCCTTC 533

RESULT 4
US-09-023-655-1112
; Sequence 1112, Application US/09023655
; Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1112:
SEQUENCE CHARACTERISTICS:
LENGTH: 968 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g184413
US-09-023-655-1112
Query Match 4.8%; Score 120; DB 3; Length 968;
Best Local Similarity 98.9%; Pred. No. 9.6e-49;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 530 GCGCGCAAGCCCAAGTGGCTGTATGCTACCGCGGGAGGACAAAGACGTTCTACCCCGAG 589
Db 525 GCGCGCAAGCCCAAGTGGCTGTATGCTACCGCGGGAGGACAAAGACGTTCTACCCCGAG 584
QY 590 GAGATCTCGTCCATGCTGCTGAGCAAGATGAAGAGAGCGCGCGAGCGTACTGGGCCAG 649
Db 585 GAGATCTCGTCCATGCTGCTGAGCAAGATGAAGAGAGCGCGCGAGCGTACTGGGCCAG 644
QY 650 CCGGTGAAGCAGCAGTGTATCACCGTGCACCTATTTTCAGTAACTCGCAGCGCCAGCC 709
Db 645 CCGGTGAAGCAGCAGTGTATCACCGTGCACCTATTTTCAGTAACTCGCAGCGCCAGCC 704
QY 710 ACCAAGACGCGGGGCCATCGCGGGCTCAAGGTGCTGCGGATCATCAATGAGGCCAG 769
Db 705 ACCAAGACGCGGGGCCATCGCGGGCTCAAGGTGCTGCGGATCATCAATGAGGCCAG 764
QY 770 GCAGCAGCCATCGCCTATGGGTGGACCGCGG 802
Db 765 GCAGCAGCCATCGCCTATGGGTGGACCGCGG 797

RESULT 5
US-09-376-774-3
; Sequence 3, Application US/09376774

; Patent No. 6759236
; GENERAL INFORMATION:
; APPLICANT: Fung, Yuen Kai
; APPLICANT: Gomer, Charles
; APPLICANT: T'Ang, Anne
; TITLE OF INVENTION: Methods To Enhance And Confine Expression
; TITLE OF INVENTION: Of Genes
; FILE REFERENCE: D6087
; CURRENT APPLICATION NUMBER: US/09/376,774
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/096,947
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 3
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: gene
; OTHER INFORMATION: heat shock response element of human heat shock 70
; OTHER INFORMATION: gene promoter
US-09-376-774-3

Query Match 4.0%; Score 100; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 7e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 60
Db 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 60

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100

RESULT 6

US-09-185-243-1

; Sequence 1, Application US/09185243

; Patent No. 6709858

; GENERAL INFORMATION:

; APPLICANT: Tsang, Tom

; APPLICANT: Gerner, Eugene W.

; APPLICANT: Harris, David T.

; APPLICANT: Hersh, Evan

; TITLE OF INVENTION: Hyperthermic Inducible Expression Vectors for Gene

; TITLE OF INVENTION: Therapy and Methods of Use Thereof

; FILE REFERENCE: 15907-0016

; CURRENT APPLICATION NUMBER: US/09/185,243

; CURRENT FILING DATE: 1998-11-03

; EARLIER APPLICATION NUMBER: US 60/064,088

; EARLIER FILING DATE: 1997-11-03

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 469

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-185-243-1

Query Match 4.0%; Score 100; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 60
Db 246 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 305

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 306 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 345

RESULT 7

US-09-398-522-111

; Sequence 111, Application US/09398522

; Patent No. 6783933

; GENERAL INFORMATION:

; APPLICANT: Issa, Jean-Pierre

; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR

; FILE REFERENCE: JHU1590

; CURRENT APPLICATION NUMBER: US/09/398,522

; CURRENT FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 120

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 111

; LENGTH: 550

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: gene

; LOCATION: (0)...(0)

; OTHER INFORMATION: HSPA6 CpG Island

US-09-398-522-111

Query Match 4.0%; Score 100; DB 3; Length 550;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 60
Db 336 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 395

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 396 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 435

RESULT 8

US-09-376-774-5

; Sequence 5, Application US/09376774

; Patent No. 6759236

; GENERAL INFORMATION:

; APPLICANT: Fung, Yuen Kai

; APPLICANT: Gomer, Charles

; APPLICANT: T'Ang, Anne

; TITLE OF INVENTION: Methods To Enhance And Confine Expression

; FILE REFERENCE: D6087

; CURRENT APPLICATION NUMBER: US/09/376,774

; CURRENT FILING DATE: 2003-03-21

; PRIOR APPLICATION NUMBER: 60/096,947

; PRIOR FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 5

; SEQ ID NO 5

; LENGTH: 10728

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: recombinant vector pDATH-TNF?

US-09-376-774-5

Query Match 4.0%; Score 100; DB 3; Length 10728;
Best Local Similarity 100.0%; Pred. No. 8e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 60
Db 6 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGGCGGAAGTTTCGCGGCG 65

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 66 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 105

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RESULT 9
US-09-513-999C-14057
; Sequence 14057, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14057
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 71
; OTHER INFORMATION: s=g or c
US-09-513-999C-14057

Query Match          3.4%; Score 85; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.8e-31;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GGCAGCAGCCTCGTGGCTTCAGCATCCGACACGAAGCTTCAGCCATGCAGGCCCCACG 246
Db 72 GGCAGCAGCCTCGTGGCTTCAGCATCCGACACGAAGCTTCAGCCATGCAGGCCCCACG 131

QY 247 GAGCTCGCGTGGCATCGACCTG 271
Db 132 GGAGCTCGCGTGGCATCGACCTG 156

RESULT 10
US-08-797-358B-1
; Sequence 1, Application US/08797358B
; Patent No. 6268478
; GENERAL INFORMATION:
; APPLICANT: Adams, John
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,358B
; FILING DATE: 11-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,491
; FILING DATE: 12-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CE 3165
; TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-797-358B-1

Query Match          2.8%; Score 71; DB 3; Length 2394;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1491 GCCACTATCCCAACCAAGCAGACCCAGACTTTCACCACTTCTCGGACAAACCGCTGGG 1550
Db 1512 GCCACTATCCCAACCAAGCAGACCCAGACTTTCACCACTTCTCGGACAAACCGCTGGG 1571

QY 1551 GTCTTCATCCA 1561
Db 1572 GTCTTCATCCA 1582

RESULT 11
US-09-936-506-3
; Sequence 3, Application US/09936506
; Patent No. 7034142
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; APPLICANT: Coste, Herve J-C
; APPLICANT: Ellis, Jonathan H
; TITLE OF INVENTION: Expression
; FILE REFERENCE: PF3623/WO
; CURRENT APPLICATION NUMBER: US/09/936,506
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: GB 9905498.3
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-936-506-3

Query Match          2.3%; Score 58; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.9e-18;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 GCGGGCTGGCGGCGAGAGAAACCGCAGGAGAGACCTCACTGCTGAGCGCCCTCGACG 179
Db 11 GCGGGCTGGCGGCGAGAGAAACCGCAGGAGAGACCTCACTGCTGAGCGCCCTCGACG 68

RESULT 12
US-10-131-827-2255
; Sequence 2255, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN-
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
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; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2255
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2255

Query Match      2.0%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGGAGCTGGAGCAAAATCT 2040
Db 1 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGGAGCTGGAGCAAAATCT 50

RESULT 13
US-10-131-831-2255
; Sequence 2255, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2255
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2255

Query Match      2.0%; Score 50; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGGAGCTGGAGCAAAATCT 2040
Db 1 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGGAGCTGGAGCAAAATCT 50

RESULT 14
US-10-171-389-185
; Sequence 185, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human hsp70B gene
US-08-171-389-185

Query Match      1.8%; Score 45; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGGCGGCGGAGGCTCTCGACTGGCGGCGGAGGCTGGCGGAGCT 52
Db 1 GGGCGGCGGAGGCTCTCGACTGGCGGCGGAGGCTGGCGGAGCT 45

RESULT 15
US-08-123-936-185
; Sequence 185, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,936
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human hsp70B gene
;
US-08-123-936-185

Query Match      1.8%; Score 45; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GGCGGGGGGGAGGCTCTCGACTGGGGGGAGGTGGGGAGGT 52
Db      1 GGCGGGGGGGAGGCTCTCGACTGGGGGGAGGTGGGGAGGT 45

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System

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Perfect score: 2493
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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	495	19.9	2361	3	US-09-925-302-281 Sequence 281, App
2	495	19.9	2361	3	US-09-925-302-281 Sequence 281, App
3	484	19.4	2336	6	US-09-919-039-203 Sequence 203, App
4	431	17.3	2962	6	US-10-002-600-97 Sequence 97, Appl
5	431	17.3	2962	10	US-10-765-700-72 Sequence 72, Appl
6	429	17.2	531	8	US-10-637-855-217 Sequence 217, App
7	329	13.2	2492	3	US-09-968-007A-527 Sequence 527, App
8	329	13.2	2492	9	US-10-278-698-290 Sequence 290, App
9	329	13.2	2492	9	US-10-278-698-804 Sequence 804, App
10	329	13.2	2492	10	US-10-843-641A-6997 Sequence 6997, App
11	283	11.4	1932	8	US-10-755-889-395 Sequence 395, App
12	260	10.4	819	6	US-10-027-632-170807 Sequence 170807, App
13	260	10.4	819	7	US-10-027-632-170807 Sequence 170807, App
14	259	10.4	397	4	US-09-925-065A-12443 Sequence 12443, A
15	259	10.4	397	5	US-09-925-065A-12443 Sequence 12443, A
16	259	10.4	397	12	US-10-301-480-113680 Sequence 113680, App
17	259	10.4	397	12	US-10-301-480-727089 Sequence 727089, App

C 18	253	10.1	777	6	US-10-027-632-168525	Sequence 168525, App
C 19	253	10.1	777	6	US-10-027-632-168526	Sequence 168526, App
C 20	253	10.1	777	7	US-10-027-632-168525	Sequence 168525, App
C 21	253	10.1	777	7	US-10-027-632-168526	Sequence 168526, App
C 22	120	4.8	968	8	US-10-641-643-1112	Sequence 1112, App
C 23	104	4.2	276	9	US-10-425-115-87729	Sequence 87729, A
C 24	100	4.0	286	6	US-10-096-549-4	Sequence 4, Appli
C 25	100	4.0	286	10	US-10-864-102-4	Sequence 4, Appli
C 26	100	4.0	469	7	US-10-152-577-1	Sequence 1, Appli
C 27	100	4.0	469	10	US-10-108-486-1	Sequence 1, Appli
C 28	100	4.0	469	11	US-10-733-280-1	Sequence 1, Appli
C 29	100	4.0	550	9	US-10-930-301-111	Sequence 111, App
C 30	100	4.0	592	6	US-10-172-399-13	Sequence 13, Appl
C 31	100	4.0	592	10	US-10-501-756-22	Sequence 22, Appl
C 32	100	4.0	714	9	US-10-489-136-27	Sequence 27, Appl
C 33	99	4.0	370	4	US-09-925-065A-561882	Sequence 561882, App
C 34	99	4.0	370	5	US-09-925-065A-561882	Sequence 561882, App
C 35	79	3.2	268	9	US-10-425-115-1630	Sequence 1630, App
C 36	76	3.0	475	3	US-09-918-995-31483	Sequence 31483, A
C 37	60	2.4	60	3	US-09-908-975-11556	Sequence 11556, A
C 38	58	2.3	119	15	US-11-167-614-3	Sequence 3, Appli
C 39	50	2.0	50	7	US-10-131-827-2255	Sequence 2255, App
C 40	48	1.9	768	9	US-10-363-345A-20773	Sequence 20773, A
C 41	48	1.9	768	9	US-10-363-345A-20773	Sequence 20773, A
C 42	48	1.9	768	10	US-10-363-483A-20773	Sequence 20773, A
C 43	48	1.9	768	10	US-10-363-483A-20773	Sequence 20773, A
C 44	45	1.8	45	3	US-09-993-346-185	Sequence 185, App
C 45	42	1.7	53	3	US-09-993-346-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-09-925-302-281
; Sequence 281, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2352)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2355)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-281

Query Match 19.9%; Score 495; DB 3; Length 2361;
Best Local Similarity 99.8%; Pred. No. 4.6e-250;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 134 GCAGAGAACCCGAGGAGAGCCCTCCTGCTGAGCCCTCGAGCGGCGGAGCGGAGCA 193
DB 72 GCAGAGAACCCGAGGAGAGCCCTCCTGCTGAGCCCTCGAGCGGCGGAGCGGAGCA 131

Qy	194	GCCTCGTGCGCTCCAGATCCGACAAGAAGCTTCAGCCATCAGCGCCCCACGGAGCTC	253
Db	132	GCCTCGTGCGCTCCAGATCCGACAAGAAGCTTCAGCCATCAGCGCCCCACGGAGCTC	191
Qy	254	GGGTGGGCATCGACTGGGCACCACTTACTCGTGTGTGGGTGTTCAGCAGGGCCGC	313
Db	192	GGGTGGGCATCGACTGGGCACCACTTACTCGTGTGTGGGTGTTCAGCAGGGCCGC	251
Qy	314	GTGAGATCTGTGGCAACGACAGGGCAACGGCACCGCACCGCCAGCTACGTGGCTTCACC	373
Db	252	GTGAGATCTGTGGCAACGACAGGGCAACGGCACCGCACCGCCAGCTACGTGGCTTCACC	311
Qy	374	GACACCGAGCGGTGTGTGGGGAACGGCGCACGAAGAGCCAGCGCGCCTGTAACCCCCACAC	433
Db	312	GACACCGAGCGGTGTGTGGGGAACGGCGCACGAAGAGCCAGCGCGCCTGTAACCCCCACAC	371
Qy	434	ACCGTGTTCATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGGACACACCGGTGCAGTGC	493
Db	372	ACCGTGTTCATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGGACACACCGGTGCAGTGC	431
Qy	494	GACATGAAGCACTGGGCCCTTCACAGTGTGTAGCGAGGGCGGCAAGCCCAAGGTGCGCGTA	553
Db	432	GACATGAAGCACTGGGCCCTTCCGGGTGTGTAGCGAGGGCGGCAAGCCCAAGGTGCGCGTA	491
Qy	554	TGCTACCGCGGGAGGACAGACGTTCACCCCGAGGAGATCTCGTCCATGTGTCTGAGC	613
Db	492	TGCTACCGCGGGAGGACAGACGTTCACCCCGAGGAGATCTCGTCCATGTGTCTGAGC	551
Qy	614	AAGATGAAGGAGACGGCGGAGGCGTACTCTGGGCCAGCCCGGTGAGCAGCGAGTGCACC	673
Db	552	AAGATGAAGGAGACGGCGGAGGCGTACTCTGGGCCAGCCCGGTGAGCAGCGAGTGCACC	611
Qy	674	GTGCCC	679
Db	612	GTGCCC	617

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RESULT 2
US-09-925-302-281
US-09-925-302-281
; Sequence 281, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2352)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2355)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-302-281
Query Match
Best Local Similarity 19.9%; Score 495; DB 3; Length 2361;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	134	GCAGAGAAACCGCAGGAGAGCCTCACTGCTGAGCGCCCTTCAGCGGCGGAGCGGCAGCA	193
Db	72	GCAGAGAAACCGCAGGAGAGCCTCACTGCTGAGCGCCCTTCAGCGGCGGAGCGGCAGCA	131
QY	194	GCCTCCGTGGCCTCCAGCATCCGACAAAGACTTCAGCCATGCAAGCCCGCCACCGGAGCTC	253
Db	132	GCCTCCGTGGCCTCCAGCATCCGACAAAGACTTCAGCCATGCAAGCCCGCCACCGGAGCTC	191
QY	254	CGGTGGGCATCGACCTGGGACACCTACTCTGCTGGGTGGCGCTGTTTCAGCAGGGCGCG	313
Db	192	CGGTGGGCATCGACCTGGGACACCTACTCTGCTGGGTGGCGCTGTTTCAGCAGGGCGCG	251
QY	314	GTGAGATTCCTGGCCAAACGACCAAGGCAACCGCACACCGCCAGCTACGTGGCTTCACCC	373
Db	252	GTGAGATTCCTGGCCAAACGACCAAGGCAACCGCACACCGCCAGCTACGTGGCTTCACCC	311
QY	374	GACACCGAGCGGTGTCGGGACCGCGGCCAAGAGCCAGCGGCCCTGAAACCCCAAC	433
Db	312	GACACCGAGCGGTGTCGGGACCGCGGCCAAGAGCCAGCGGCCCTGAAACCCCAAC	371
QY	434	ACCGTGTTCGATGTCGAAGCGCTGATCGGGCGCAAGTTCGCGGACACCAACGTCAGTCG	493
Db	372	ACCGTGTTCGATGTCGAAGCGCTGATCGGGCGCAAGTTCGCGGACACCAACGTCAGTCG	431
QY	494	GACATGAAGCATGCGCCCTTCAGTGTGTGACGAGGCGCAGGCCCAAGGTGCGCGTA	553
Db	432	GACATGAAGCATGCGCCCTTCAGTGTGTGACGAGGCGCAGGCCCAAGGTGCGCGTA	491
QY	554	TGCTACCGCGGGAGGACAAAGACTTCTACCCCGAGGAGATCTCGTCATGGTCTGAGC	613
Db	492	TGCTACCGCGGGAGGACAAAGACTTCTACCCCGAGGAGATCTCGTCATGGTCTGAGC	551
QY	614	AAGATGAAGGAGACCGCCGAGGCTTACTTGGCGCAGCCCGTCAGCAGCTGATCACCC	673
Db	552	AAGATGAAGGAGACCGCCGAGGCTTACTTGGCGCAGCCCGTCAGCAGCTGATCACCC	611
QY	674	GTGCC	679
Db	612	GTGCC	617

```

RESULT 3
US-09-919-039-203
; Sequence 203, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 203
; LENGTH: 2336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1440032CE1
US-09-919-039-203

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Query Match	19.4%;	Score 484;	DB 3;	Length 2336;
Best Local Similarity	98.8%;	Pred. No. 3e-244;		
Matches 1404;	Conservative 0;	Mismatches 16;	Indels 1;	Gaps 1;

QY	152	GAGCCTCACTGCTGAGCGCCCTCTGACGGCGGAGCGGACGACCTTCGTCGGCTCCACG	211
Db	29	GAGCCTCACTGCTGAGCGCCCTCTGACGGCGGAGCGGACGACCTTCGTCGGCTCCACG	88
QY	212	ATCCGACACGAAGACTTCAGCCATCGAGGCCCCACGGGAGCTCGCGTGGGCATCGACCTG	271

Db 89 ATCCGACAAAGCTTTCAGCCATCAGGCCCCACGGAGCTCGCGGTGGGCATCGACCTG 148
Qy 272 GGCACCACTACTCGTGGTGGGCGTGTTCAGCAGGCGCGCTGGAGATCTTCGGCCAA 331
Db 149 GGCACCACTACTCGTGGTGGGCGTGTTCAGCAGGCGCGCTGGAGATCTTCGGCCAA 208
Qy 332 GACAGGGCAACCGCACCGCCAGCTACGTGGCTTCACCGACACCGAGCGGCTGGTC 391
Db 209 GACAGGGCAACCGCACCGCCAGCTACGTGGCTTCACCGACACCGAGCGGCTGGTC 268
Qy 392 GGGGACCGGCGCAAGAGCCAGGCGGCGCTGACCCCAACACACCGCTGTCGATGCCAAG 451
Db 269 GGGGACCGGCGCAAGAGCCAGGCGGCGCTGACCCCAACACACCGCTGTCGATGCCAAG 328
Qy 452 CGGCTGATCGGCGGCGCAAGGTCGCGGACACCAACGCTGCGATCGGACATGAAGCACTGGCCCC 511
Db 329 CGGCTGATCGGCGGCGCAAGGTCGCGGACACCAACGCTGCGATCGGACATGAAGCACTGGCCCC 388
Qy 512 TTCCAGGTGTGAGCGAGGCGGCAAGCCCAAGGTGCGCGTATGCTACCGCGGGAGGAC 571
Db 389 TTCCGCGTGTGAGCGAGGCGGCAAGCCCAAGGTGCGCGTATGCTACCGCGGGAGGAC 448
Qy 572 AAGACGTTCTACCCCGAGGAGATCTCGTCCATGCTGTGACCAAGATGAAGGAGCGGCC 631
Db 449 AAGACGTTCTACCCCGAGGAGATCTCGTCCATGCTGTGACCAAGATGAAGGAGCGGCC 508
Qy 632 GAGCGGTACCTGGGCGAGCCCGTGAAGCAGCAGTATCAACGCTGCCACCTATTTTCAGT 691
Db 509 GAGCGGTACCTGGGCGAGCCCGTGAAGCAGCAGTATCAACGCTGCCACCTATTTTCAGT 568
Qy 692 AACTCGCAGCGCCAGGCCACCAAGAGCGCGGGGCCATCGCGGGGCTCAAGGTGCTGCCG 751
Db 569 GACTCGCAGCGCCAGGCCACCAAGAGCGCGGGGCCATCGCGGGGCTCAACGTGTTGCGG 628
Qy 752 ATCATCAATGAGGCGCAGCGACGACCATGCTCTATGCGGTGACCGCGGGCGCGGGA 811
Db 629 ATCATCAATGAGGCGCAGCGACGCTGCCATGCTCTATGCGGTGACCGCGGGCGCGGGA 688
Qy 812 AAGCGCAACGTGCTCATTTTGAACCTGGGTGGGGGACCTTCGATGTCGCTTCTCC 871
Db 689 GAGCGCAACGTGCTCATTTTGAACCTGGGTGGGGGACCTTCGATGTCGCTTCTCC 748
Qy 872 ATTGACCGCGGTGTCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAG 931
Db 749 ATTGACCGGTGTCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAG 808
Qy 932 GACTTCGACACCGGCTCGTGAACCACTTCATGGAAGATTCGGCGGGAAGCATGGGAAG 991
Db 809 GACTTCGACACCGGCTCGTGAACCACTTCATGGAAGATTCGGCGGGAAGCATGGGAAG 868
Qy 992 GACTGAGCGGGAACAAGCGTGCCTGCGCAGGCTGCGCACAGCCTGTGAGCGGCCAAG 1051
Db 869 GACTGAGCGGGAACAAGCGTGCCTGCGCAGGCTGCGCACAGCCTGTGAGCGGCCAAG 928
Qy 1052 CGCACCCCGTCTTCAGCACCCAGGCCACCTCGAGATAGACTCCCTGTTTCGAGGGCGTG 1111
Db 929 CGCACCCCGTCTTCAGCACCCAGGCCACCTCGAGATAGACTCCCTGTTTCGAGGGCGTG 988
Qy 1112 GACTTCTAAGTTCATCACTCGTGGCGGCTTTGAGGAATGTGTCTCAGACCTCTTCGCG 1171
Db 989 GACTTCTAAGTTCATCACTCGTGGCGGCTTTGAGGAATGTGTCTCAGACCTCTTCGCG 1048
Qy 1172 AGCACCTCGAGCGGCTGAGAGAGGCGCTCGGGATGCGCAAGCTGGACAGGCGCCAGATT 1231
Db 1049 AGCACCTCGAGCGGCTGAGAGAGGCGCTCGGGATGCGCAAGCTGGACAGGCGCCAGATT 1108
Qy 1232 CATGACTTCGTTCTGGGGGAGGGGCTCCACTCGCATCCCAAGGTGAGAAAGTTGCTGCA 1291
Db 1109 CATGAGCTGCTGTTGGTGGG-GGGCTCCACACGATCCCAAGGTGAGAAAGTTGCTGCA 1167
Qy 1292 GGACTTCTCAACGGCAAGAGCTGAACAAGAGCATCAACCTGTAGAGGCTGTGGCCTA 1351

Db 1168 GGACTTCTTCAACGCGCAAGGAGCTGAACAAGACATCAACCCCTGATGAGCTGTGGCCTA 1227
Qy 1352 TGGGTCTGCTGTGTCAGCGCGCGCTGTGATGCGGGGCAAAATGTGAGAAAGTGCAGGATCT 1411
Db 1228 TGGGGTCTGCTGTGTCAGCGCGCGCTGTGATGCGGGGCAAAATGTGAGAAAGTGCAGGATCT 1387
Qy 1412 CTTGCTGCTGATGTGTGGCTCCCTGCTCTCTGCGGGCTGGAGACAGCAGGTGGGGTGTGAC 1471
Db 1288 CTTGCTGCTGATGTGTGGCTCCCTGCTCTCTGCGGGCTGGAGACAGCAGGTGGGGTGTGAC 1347
Qy 1472 CAGCTGATCCAGAGAAAGCCCACTATCCCAACCAAGCAGACCCAGACTTTTACCACTTA 1531
Db 1348 CAGCTGATCCAGAGAAAGCCCACTATCCCAACCAAGCAGACCCAGACTTTTACCACTTA 1407
Qy 1532 CTGCGAACCAAGCCCTGGGGTCTTCATCCAGGTGTATGAGG 1572
Db 1408 CTGCGAACCAAGCCCTGGGGTCTTCATCCAGGTGTATGAGG 1448

RESULT 4
US-10-002-600-97
; Sequence 97, Application US/10002600
; Publication No. US20020137077A1
; GENERAL INFORMATION:
; APPLICANT: Hopkins, Christopher M.
; APPLICANT: Peterson, David P.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS
; FILE REFERENCE: PA-0042 US
; CURRENT APPLICATION NUMBER: US/10/002,600
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/243,521
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PERL Program
; SEQ ID NO 97
; LENGTH: 2962
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Template ID: 349676.8
US-10-002-600-97

Query Match 17.3%; Score 431; DB 6; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3e-216;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 198 CGTGGCTTCCAGCATCCGACAAAGAGCTTCAGCCATGAGGCCCAACCGGAGCTCGCGG 257
Db 699 CGTGGCTTCCAGCATCCGACAAAGAGCTTCAGCCATGAGGCCCAACCGGAGCTCGCGG 758
Qy 258 TGGGATCGACCTGGGACCACTACTCTGCTGGGCGTGTTCAGAGGGCGCGTGG 317
Db 759 TGGGATCGACCTGGGACCACTACTCTGCTGGGCGTGTTCAGAGGGCGCGTGG 818
Qy 318 AGATCTGCGCAACGACGAGGCAACCGCACCGCCAGCTACGTGGCTTCACCGACA 377
Db 819 AGATCTGCGCAACGACGAGGCAACCGCACCGCCAGCTACGTGGCTTCACCGACA 878
Qy 378 CGAGCGGCTGTTCGGGAGACGGCGCAAGAGCGCGGCGCCCTGAAACCCCAACACCG 437
Db 879 CGAGCGGCTGTTCGGGAGACGGCGCAAGAGCGCGGCGCCCTGAAACCCCAACACCG 938
Qy 438 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTCGCGACACCAAGGTGCGATGCGACA 497
Db 939 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTCGCGACACCAAGGTGCGATGCGACA 998
Qy 498 TGAAGCACTGGCCCTTCGCGGTGGTGAAGCGGGCGCAAGCCCAAGGTGCGGTATGCT 557
Db 999 TGAAGCACTGGCCCTTCGCGGTGGTGAAGCGGGCGCAAGCCCAAGGTGCGGTATGCT 1058

QY	558	ACCGGGGAGAGACAAGAGCTTCTACCCGAGGAGATCTCGTCCATGCTCTCAGCAAGA	617
Db	1059	ACCGGGGAGGAGACAAGAGCTTCTACCCGAGGAGATCTCGTCCATGCTCTGAGCAAGA	1118
QY	618	TGAAGGAGACGCCGAGGCGGTACCTTGGGCCAGCCCGTGAAGACGCGAGTGAATCACCGTGC	677
Db	1119	TGAAGGAGACGCCGAGGCGGTACCTTGGGCCAGCCCGTGAAGACGCGAGTGAATCACCGTGC	1178
QY	678	CC 679	
Db	1179	CC 1180	
RESULT 5			
US-10-765-700-72			
; Sequence 72, Application US/10765700			
; Publication No. US20050130171A1			
; GENERAL INFORMATION:			
; APPLICANT: Loring, Jeanne F.			
; APPLICANT: Tingley, Debora W.			
; APPLICANT: Edwards, Carla M.			
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE			
; FILE REFERENCE: PA-0024 US			
; CURRENT APPLICATION NUMBER: US/10/765,700			
; CURRENT FILING DATE: 2004-01-26			
; PRIOR APPLICATION NUMBER: US/09/566,921			
; PRIOR FILING DATE: PRIOR FILING DATE: 2000-05-05			
; NUMBER OF SEQ ID NOS: 138			
; SOFTWARE: PERL Program			
; SEQ ID NO 72			
; LENGTH: 2962			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: Incyte ID No: 349676.8			
US-10-765-700-72			
Query Match 17.3%; Score 431; DB 10; Length 2962;			
Best Local Similarity 99.8%; Pred. No. 3e-216;			
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	198	CGTGGCTCCAGCATCCGACAAGAGCTTCAGCCATGACAGGCCCCACCGGAGCTCGCGG	257
Db	699	CGTGGCTCCAGCATCCGACAAGAGCTTCAGCCATGACAGGCCCCACCGGAGCTCGCGG	758
QY	258	TGGGATCGACTGGGACACCACTACTCTGCTGGGCGTGTTCAGCAGGCGCGGTGG	317
Db	759	TGGGATCGACTGGGACACCACTACTCTGCTGGGCGTGTTCAGCAGGCGCGGTGG	818
QY	318	AGATCTGGCCAAACGACAGGGCAACCGCACCGCCAGCTACGTGGCCTTCACCGACA	377
Db	819	AGATCTGGCCAAACGACAGGGCAACCGCACCGCCAGCTACGTGGCCTTCACCGACA	878
QY	378	CGAGCGGCTGTTCGGGAGCGGGCAAGAGACAGGCGGCGCTTGAACCCCAACACCG	437
Db	879	CGAGCGGCTGTTCGGGAGCGGGCAAGAGACAGGCGGCGCTTGAACCCCAACACCG	938
QY	438	TGTTCCATGCCAAGCGGCTGTATCGGGCGAAAGTTTCGGGACACACCGTGCAGTCGACA	497
Db	939	TGTTCCATGCCAAGCGGCTGTATCGGGCGAAAGTTTCGGGACACACCGTGCAGTCGACA	998
QY	498	TGAAGACATGGCCCTTCAGAGTGTGTGAGGAGGGCGGCAAGCCCAAGTGGCGTATGCT	557
Db	999	TGAAGACATGGCCCTTCAGAGTGTGTGAGGAGGGCGGCAAGCCCAAGTGGCGTATGCT	1058
QY	558	ACCGGGGAGGACAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGCTCTGAGCAAGA	617
Db	1059	ACCGGGGAGGACAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGCTCTGAGCAAGA	1118
QY	618	TGAAGGAGACGCCGAGGCGGTACCTTGGGCCAGCCCGTGAAGACGCGAGTGAATCACCGTGC	677
Db	1119	TGAAGGAGACGCCGAGGCGGTACCTTGGGCCAGCCCGTGAAGACGCGAGTGAATCACCGTGC	1178

;; TITLE OF INVENTION: Gene Sets
;; FILE REFERENCE: 689290-71
;; CURRENT APPLICATION NUMBER: US/09/968,007A
;; CURRENT FILING DATE: 2001-10-02
;; PRIOR APPLICATION NUMBER: US/60/237,172
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: US/60/237,173
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: US/60/237,278
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: US/60/237,294
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: US/60/237,295
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: US/60/237,316
;; PRIOR FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 1001
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 527
;; LENGTH: 2492
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-968-007A-527

Query Match 13.2%; Score 329; DB 3; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 246
Db 205 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 264
Qy 247 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 306
Db 265 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 324
Qy 307 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 366
Db 325 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 384
Qy 367 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 426
Db 385 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 444
Qy 427 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 486
Db 445 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 8
US-10-278-698-290
; Sequence 290, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmueller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
; LENGTH: 2492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-290

Query Match 13.2%; Score 329; DB 3; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 246
Db 205 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 264
Qy 247 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 306
Db 265 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 324
Qy 307 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 366
Db 325 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 384
Qy 367 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 426
Db 385 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 444
Qy 427 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 486
Db 445 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

Query Match 13.2%; Score 329; DB 9; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 246
Db 205 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 264
Qy 247 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 306
Db 265 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 324
Qy 307 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 366
Db 325 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 384
Qy 367 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 426
Db 385 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 444
Qy 427 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 486
Db 445 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 9
US-10-278-698-804
; Sequence 804, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmueller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 804
; LENGTH: 2492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-804

Query Match 13.2%; Score 329; DB 9; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 246
Db 205 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCCACG 264
Qy 247 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 306
Db 265 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 324
Qy 307 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 366
Db 325 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCGCAACGACCGCAACGACCGCAACG 384
Qy 367 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 426
Db 385 CTTACCGACACCGAGCGGCTGGTGGGGACGCGGCAAGAGCCAGGCGGCGCTTGAACCC 444
Qy 427 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 486
Db 445 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGGGACACCGGT 504

Mon Nov 6 11:55:56 2006

QY 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 10

US-10-843-641A-6997
; Sequence 6997, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6997
; LENGTH: 2492
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(2492)
; OTHER INFORMATION: n=a,t,g or c

Query Match 13.2%; Score 329; DB 10; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 0

QY 187 GGCAGCAGCTCCGTGGCTCCAGATCCGACAAAGATCTCAGCCATGCGCCCCACG 246
Db 205 GGCAGCAGCTCCGTGGCTCCAGATCCGACAAAGATCTCAGCCATGCGCCCCACG 264
QY 247 GGAGCTCGCGTGGGATCGACCTGCGGACCACTACTCTGCTGGCGGTGTTTCAGCA 306
Db 265 GGAGCTCGCGTGGGATCGACCTGCGGACCACTACTCTGCTGGCGGTGTTTCAGCA 324
QY 307 GGGCGCGTGAGATCTCTGGCCACACGACGAGGCAACCGACCCAGCTACGTGGC 366
Db 325 GGGCGCGTGAGATCTCTGGCCACACGACGAGGCAACCGACCCAGCTACGTGGC 384
QY 367 CTTTACCGACACCGAGCGGCTGGTGGGAGCGCGGCAAGAGCGCGCCCTGACCC 426
Db 385 CTTTACCGACACCGAGCGGCTGGTGGGAGCGCGGCAAGAGCGCGCCCTGACCC 444
QY 427 CCACAAACCGTGTTCGATGCCAGCGGCTGATCGGGGGCAAGTTCCGGACACACCGGT 486
Db 445 CCACAAACCGGTTTCGATGCCAGCGGCTGATCGGGGGCAAGTTCCGGGACACACCGGT 504

QY 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 11

US-10-755-889-395
; Sequence 395, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 395
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-755-889-395

Query Match 11.4%; Score 283; DB 8; Length 1932;
Best Local Similarity 100.0%; Pred. No. 5e-138; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0

QY 233 ATGACGCCCCACGGAGCTCGCGGTGGGATCGACCTGGGACCACTACTCTGCTGGT 292
Db 1 ATGACGCCCCACGGAGCTCGCGGTGGGATCGACCTGGGACCACTACTCTGCTGGT 60
QY 293 GGGCTGTTTCAGCAGGCGCGGTGGGATCTGGCCAAACGACGAGGCAACGACCCACG 352
Db 61 GGGCTGTTTCAGCAGGCGCGGTGGGATCTGGCCAAACGACGAGGCAACGACCCACG 120
QY 353 CCAGCTACGTGGCTTCCACGACACCGAGCGGCTGTGGGACGCGGCAAGAGCCAG 412
Db 121 CCAGCTACGTGGCTTCCACGACACCGAGCGGCTGTGGGACGCGGCAAGAGCCAG 180
QY 413 GCGGCCCTGAACCCCAACACCGTGTTCGATGCCAGCGGCTGATCGGGCGCAAGTTC 472
Db 181 GCGGCCCTGAACCCCAACACCGTGTTCGATGCCAGCGGCTGATCGGGCGCAAGTTC 240
QY 473 GCGGACACACCGGTGCGATCGGACATGAAGCACTGGCCCTTCC 515
Db 241 GCGGACACACCGGTGCGATCGGACATGAAGCACTGGCCCTTCC 283

RESULT 12

US-10-027-632-170807
; Sequence 170807, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170807
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-170807

Query Match
Best Local Similarity 10.4%; Score 260; DB 6; Length 819;
Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 825 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTCGGTTCTCTCAATTGAGCGCGGTG 884
Db 49 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTCGGTTCTCTCAATTGAGCGGTG 108
QY 885 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAAC 944
Db 109 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAAC 168
QY 945 GGCTCGTGAACCACTTCATGGAAGAAATTCGGCGGGAAGCATGGGAAGGACCTGAGCGGGA 1004
Db 169 GGCTCGTGAACCACTTCATGGAAGAAATTCGGCGGGAAGCATGGGAAGGACCTGAGCGGGA 228
QY 1005 ACAAGCGTCCCTGCGCAGCTGCGACAGCTGTGAGCGCGCAAGCGCACCCCTGCT 1064
Db 229 ACAAGCGTCCCTGCGCAGCTGCGACAGCTGTGAGCGCGCAAGCGCACCCCTGCT 288
QY 1065 CCAGCACCCAGGCGCCCTGCGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 1124
Db 289 CCAGCACCCAGGCGCCCTGCGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 348
QY 1125 CCATCACTCGTCCCGCTTTGAGGAACCTGTGCTCAGACCTTTCGCGCAGCACCCCTGGAGC 1184
Db 349 CCATCACTCGTCCCGCTTTGAGGAACCTGTGCTCAGACCTTTCGCGCAGCACCCCTGGAGC 408
QY 1185 CGGTGGAGAGGCGCCCTGCGGATGCCAAGCTGCAAGGCCAGATTCATGAC 1237
Db 409 CGGTGGAGAGGCGCCCTGCGGATGCCAAGCTGCAAGGCCAGATTCATGAC 461
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RESULT 13
US-10-027-632-170807
; Sequence 170807, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 170807
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-170807

Query Match
Best Local Similarity 10.4%; Score 260; DB 7; Length 819;
Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 825 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTCGGTTCTCTCAATTGAGCGCGGTG 884
Db 49 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTCGGTTCTCTCAATTGAGCGGTG 108
QY 885 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAAC 944
Db 109 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAAC 168
QY 945 GGCTCGTGAACCACTTCATGGAAGAAATTCGGCGGGAAGCATGGGAAGGACCTGAGCGGGA 1004
Db 169 GGCTCGTGAACCACTTCATGGAAGAAATTCGGCGGGAAGCATGGGAAGGACCTGAGCGGGA 228
QY 1005 ACAAGCGTCCCTGCGCAGCTGCGACAGCTGTGAGCGCGCAAGCGCACCCCTGCT 1064
Db 229 ACAAGCGTCCCTGCGCAGCTGCGACAGCTGTGAGCGCGCAAGCGCACCCCTGCT 288
QY 1065 CCAGCACCCAGGCGCCCTGCGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 1124
Db 289 CCAGCACCCAGGCGCCCTGCGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 348
QY 1125 CCATCACTCGTCCCGCTTTGAGGAACCTGTGCTCAGACCTTTCGCGCAGCACCCCTGGAGC 1184
Db 349 CCATCACTCGTCCCGCTTTGAGGAACCTGTGCTCAGACCTTTCGCGCAGCACCCCTGGAGC 408
QY 1185 CGGTGGAGAGGCGCCCTGCGGATGCCAAGCTGCAAGGCCAGATTCATGAC 1237
Db 409 CGGTGGAGAGGCGCCCTGCGGATGCCAAGCTGCAAGGCCAGATTCATGAC 461
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RESULT 14

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US-09-925-065A-12443/C
; Sequence 12443, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12443
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-12443

Query Match
Best Local Similarity 10.4%; Score 259; DB 4; Length 397;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1263 CGCATCCCCCAGGTGCAGAAAGTTGCTGCAGGAGTTCTTTCACGCGCAAGGAGCTGAACAAG 1322

QY

1503

ACCAAGCAGACCCAGACTTTTCCACCACTTCTCGGACAACCAAGCCTGGGGTCTTTCATCCAG

1562

Db

116

ACCAAGCAGACCCAGACTTTTCCACCACTTCTCGGACAACCAAGCCTGGGGTCTTTCATCCAG

57

QY

1563

GTGTATGAGG

1572

Db

56

GTGTATGAGG

47

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Db

356

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297

QY

1323

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1382

Db

296

AGCATCAACCTGATGAGGCTGTGGCTATGGGTCTGCTGCAGCGCGCGTGTGTATG

237

QY

1383

GGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGTGATGTGGCTCCCTGTCTCTG

1442

Db

236

GGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGTGATGTGGCTCCCTGTCTCTG

177

QY

1443

GGGCTGAGACAGCAGGTGGGTGATGACCAACGCTGATCCAGAGAACGCCACTATCCCC

1502

Db

176

GGGCTGAGACAGCAGGTGGGTGATGACCAACGCTGATCCAGAGAACGCCACTATCCCC

117

QY

1503

ACCAAGCAGACCCAGACTTTTCCACCACTTCTCGGACAACCAAGCCTGGGGTCTTTCATCCAG

1562

Db

116

ACCAAGCAGACCCAGACTTTTCCACCACTTCTCGGACAACCAAGCCTGGGGTCTTTCATCCAG

57

QY

1563

GTGTATGAGG

1572

Db

56

GTGTATGAGG

47

RESULT 15
US-09-925-065A-12443/c
; Sequence 12443, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12443
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-12443

Query Match 10.4%; Score 259; DB 5; Length 397;
Best Local Similarity 99.7%; Pred. No. 2.5e-125;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1263

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1322

Db

356

CGCATCCCCAAGTGCAGAGTTGCTGCAGGACTTCTTCAACGCGCAAGGAGCTGAACAAG

297

QY

1323

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1382

Db

296

AGCATCAACCTGATGAGGCTGTGGCTATGGGTCTGCTGTGAGGCGCGTGTGTATG

237

QY

1383

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1442

Db

236

GGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGTGATGTGGCTCCCTGTCTCTG

177

QY

1443

GGGCTGAGACAGCAGGTGGGTGATGACCAACGCTGATCCAGAGAACGCCACTATCCCC

1502

Db

176

GGGCTGAGACAGCAGGTGGGTGATGACCAACGCTGATCCAGAGAACGCCACTATCCCC

117

GenCore version 5.1.9
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2493	100.0	2493	6	US-10-764-316-7
2	519	20.8	1276	8	US-11-266-748A-183816
3	519	20.8	1276	8	US-11-266-748A-240242
4	400	16.0	702	8	US-11-266-748A-100981
5	400	16.0	702	8	US-11-266-748A-153792
6	283	11.4	1932	6	US-10-511-937-2830
7	227	9.1	777	8	US-11-266-748A-358486
8	227	9.1	777	8	US-11-266-748A-41865
9	187	7.5	445	6	US-10-834-268-4047
10	187	7.5	445	6	US-11-266-748A-52935
11	187	7.5	1000	8	US-11-266-748A-221107
12	187	7.5	1000	8	US-11-266-748A-395612
13	187	7.5	1000	8	US-11-266-748A-466658
14	167	6.7	559	8	US-11-266-748A-13932
15	143	5.7	682	8	US-11-266-748A-56036
16	120	4.8	968	6	US-10-764-316-9
17	100	4.0	729	8	US-11-266-748A-391479
18	100	4.0	729	8	US-11-266-748A-482197
19	91	3.7	445	6	US-10-834-268-4097
20	50	2.0	50	6	US-10-511-937-2661
21	38	1.5	1817	8	US-11-293-697-2173
22	38	1.5	2496	8	US-11-266-748A-30574
23	34	1.4	391	8	US-11-266-748A-169838

24 1.4 951 8 US-11-266-748A-381019 Sequence 381019,
25 1.4 951 8 US-11-266-748A-430773 Sequence 430773,
26 1.4 957 8 US-11-266-748A-23277 Sequence 23277, A
27 1.4 960 8 US-11-266-748A-184820 Sequence 184820,
28 1.4 960 8 US-11-266-748A-192321 Sequence 192321,
29 1.4 1119 8 US-11-266-748A-251463 Sequence 251463,
30 1.4 1119 8 US-11-266-748A-275460 Sequence 275460,
31 1.4 1119 8 US-11-266-748A-311980 Sequence 311980,
32 1.4 1613 8 US-11-266-748A-184822 Sequence 184822,
33 1.4 1613 8 US-11-266-748A-184822 Sequence 184822,
34 1.4 2563 8 US-11-266-748A-251465 Sequence 251465,
35 1.4 2563 8 US-11-266-748A-275462 Sequence 275462,
36 1.4 2563 8 US-11-266-748A-311982 Sequence 311982,
37 1.4 5387 6 US-10-517-441-111 Sequence 111, App
38 1.4 4647455 6 US-10-641-321-205 Sequence 205, App
39 1.3 2152 6 US-10-953-349-38921 Sequence 38921, A
40 1.3 2152 9 US-11-056-355B-1264 Sequence 1264, Ap
41 1.3 2168 9 US-11-174-307B-4949 Sequence 4949, Ap
42 29 1.2 813 9 US-11-218-305-2522 Sequence 2522, Ap
43 29 1.2 2315 6 US-10-953-349-31228 Sequence 31228, A
44 28 1.1 924 8 US-11-266-748A-184821 Sequence 184821,
45 28 1.1 924 8 US-11-266-748A-192322 Sequence 192322,

ALIGNMENTS

RESULT 1

US-10-764-316-7
; Sequence 7, Application US/10764316
; Publication No. US20060127359A1
; GENERAL INFORMATION:
; APPLICANT: BORRELLI, MICHAEL J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT ACTIVATED GENE
; FILE REFERENCE: 10546-109
; CURRENT APPLICATION NUMBER: US/10/764,316
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,473
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 2493
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-316-7

Query Match 100.0%; Score 2493; DB 6; Length 2493;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGGGCGGGCGGGAGGCTTCGACTGGCGGGAGAGGTTCGGGAGAGGTTTCGGCGG 60
DB 1 CCCGGGCGGGCGGGAGGCTTCGACTGGCGGGAGAGGTTCGGGAGAGGTTTCGGCGG 60
QY 61 GCGGGGTTCGGGGAGGTTCGAAAGAGGTGAAACCGTTCGAGCGGAGCTGACGAGATCCG 120
DB 61 GCGGGGTTCGGGGAGGTTCGAAAGAGGTGAAACCGTTCGAGCGGAGCTGACGAGATCCG 120
QY 121 AGCCGGGCTGGCGGCAGAGAAACCGCAGGAGAGCTCTACTGTGAGCGCCCTCGACCG 180
DB 121 AGCCGGGCTGGCGGCAGAGAAACCGCAGGAGAGCTCTACTGTGAGCGCCCTCGACCG 180
QY 181 CGGAGCGGAGCAGCCTTCGTTGGCTTCAGACTCCAGCAAGAGCTTCAGCCATGCGGC 240
DB 181 CGGAGCGGAGCAGCCTTCGTTGGCTTCAGACTCCAGCAAGAGCTTCAGCCATGCGGC 240
QY 241 CCCAGGGAGCTCGGGTGGGCATCGACTGGGACCACTACTCTGTCGTCGGCGGTGT 300
DB 241 CCCAGGGAGCTCGGGTGGGCATCGACTGGGACCACTACTCTGTCGTCGGCGGTGT 300
QY 301 TCAGAGGGCGGCTGGAGATCTTGCCAAACGACGAGGCAACCGCACCAGCCAGCTA 360

301	Db	TCAGCAGGGCGCGTGGAGATCTTGGCCAAAGACACAGGCGCAACCGCACCGCCAGCTA	360
361	Qy	CGTGGCCTTCAACCGACACCGAGCGGTGTGCGGGACGCGGCCAAGAGCGCAGCGGGCCCT	420
361	Db	CGTGGCCTTCAACCGACACCGAGCGGTGTGCGGGACGCGGCCAAGAGCGCAGCGGGCCCT	420
421	Qy	GAACCCCAACAACCGGTGTGATGCCAAGCGCTGATCGGGCGCAAGTTTCGCGGACAC	480
421	Db	GAACCCCAACAACAACCGGTGTGATGCCAAGCGCTGATCGGGCGCAAGTTTCGCGGACAC	480
481	Qy	CACGCTGCAGTCGACATGAAGCACTGGCCCTTCCAGGTGGTGAGCGGGCGGCAAGCC	540
481	Db	CACGCTGCAGTCGACATGAAGCACTGGCCCTTCCAGGTGGTGAGCGGGCGGCAAGCC	540
541	Qy	CAAGTGGCGTATGCTTACCGCGGGAGGACAGACGTCTTACCCGAGAGATCTCGTC	600
541	Db	CAAGTGGCGTATGCTTACCGCGGGAGGACAGACGTCTTACCCGAGAGATCTCGTC	600
601	Qy	CATGTGTCTGAGCAAGATGAAGGAGACGGCCGAGCGGTACTTGGCGACGCCGTGAAGCA	660
601	Db	CATGTGTCTGAGCAAGATGAAGGAGACGGCCGAGCGGTACTTGGCGACGCCGTGAAGCA	660
661	Qy	CGCAGTGAATCAACCGTGCACCTATTTCAGTAACTCTCGAGCGCCAGCCACCAAGGACGC	720
661	Db	CGCAGTGAATCAACCGTGCACCTATTTCAGTAACTCTCGAGCGCCAGCCACCAAGGACGC	720
721	Qy	GGGGGCCATCGCGGGCTCAAGGTGCTCCGATCATCAATGAGGCCACGCGAGCGCAT	780
721	Db	GGGGGCCATCGCGGGCTCAAGGTGCTCCGATCATCAATGAGGCCACGCGAGCGCAT	780
781	Qy	CGCCTATGGCTGGACCGCGGGCGCGGGAAGCGCAACGTGCTCATTTTGACCTGGG	840
781	Db	CGCCTATGGCTGGACCGCGGGCGCGGGAAGCGCAACGTGCTCATTTTGACCTGGG	840
841	Qy	TGGGGCACTTCGATGTGCGTCTCTCCATTCAGCGCCGCTGTCTTTGAGGTGAAGC	900
841	Db	TGGGGCACTTCGATGTGCGTCTCTCCATTCAGCGCCGCTGTCTTTGAGGTGAAGC	900
901	Qy	CACCTGTGGAGATACCCACCTGGGAGGAGACCTTCGACACCGGCTCGTGAACCACTT	960
901	Db	CACCTGTGGAGATACCCACCTGGGAGGAGACCTTCGACACCGGCTCGTGAACCACTT	960
961	Qy	CATGGAGATTCGGCGGAAGCATGGGAGGACCTGAGCGGGAAACAAGCTGCGCTCGC	1020
961	Db	CATGGAGATTCGGCGGAAGCATGGGAGGACCTGAGCGGGAAACAAGCTGCGCTCGC	1020
1021	Qy	CAGGCTCGCACAGCCTGTGAGCGCGCAAGCGCACCCGCTCTCCAGCACCCAGGCCAC	1080
1021	Db	CAGGCTCGCACAGCCTGTGAGCGCGCAAGCGCACCCGCTCTCCAGCACCCAGGCCAC	1080
1081	Qy	CCTGGAGATAGACTCCCTGTTCAGAGCGGTGGACTTCTCAAGTCCATCACTCGTCCCG	1140
1081	Db	CCTGGAGATAGACTCCCTGTTCAGAGCGGTGGACTTCTCAAGTCCATCACTCGTCCCG	1140
1141	Qy	CTTTGAGGAACTGTGCTCAGACCTCTTCGCGAGCACCTTCGAGCGCGGTGGAGAGCCCT	1200
1141	Db	CTTTGAGGAACTGTGCTCAGACCTCTTCGCGAGCACCTTCGAGCGCGGTGGAGAGCCCT	1200
1201	Qy	GCGGATGCGAAGCTGGACAGGCCAGATTCATGACTTCGTCTCGGGGGAGGGCTCCA	1260
1201	Db	GCGGATGCGAAGCTGGACAGGCCAGATTCATGACTTCGTCTCGGGGGAGGGCTCCA	1260
1261	Qy	CTTCGATCCCAAGGTGACAGAGTTGTGCAAGGACTTCTTCAACCGGCAAGGAGCTGAACA	1320
1261	Db	CTTCGATCCCAAGGTGACAGAGTTGTGCAAGGACTTCTTCAACCGGCAAGGAGCTGAACA	1320
1321	Qy	AGAGCATCAACCTGATGAGGCTGCGCTATGGGTCTGCTGTGAGCGCGCGCTGTGA	1380
1321	Db	AGAGCATCAACCTGATGAGGCTGCGCTATGGGTCTGCTGTGAGCGCGCGCTGTGA	1380
1381	Qy	TGGGGGACAAATGTGAGAAAGTGCAGGATCTCTCTGCTGCTGGATGTGGCTCCCTGCTC	1440

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RESULT 2
US-11-266-748A-183816/c
; Sequence 183816, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 183816
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1066)..(1090)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-183816

Query Match 20.8%; Score 519; DB 8; Length 1276;
Best Local Similarity 99.7%; Pred. No. 2.5e-251;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGCGGGCGGGCGGGAGGCTTCGACTGGGGCGGAAGGTTCGGGAAGGTTTCGGCGG 60
Db 726 CCCGGCGGGCGGGCGGGAGGCTTCGACTGGGGCGGAAGGTTCGGGAAGGTTTCGGCGG 667

QY 61 GCGGGGTTCGGGGAGGTGCAAAAGGATGAAAGCCCTGGAAGCGGAGCTGAGCAGATCCG 120
Db 666 GCGGGGTTCGGGGAGGTGCAAAAGGATGAAAGCCCTGGAAGCGGAGCTGAGCAGATCCG 607

QY 121 AGCCGGCTTCGGCGCAGAGAAACCGCAGGAGAGCTTCAGTCTGAGCGCCCTCCAGCG 180
Db 606 AGCCGGCTTCGGCGCAGAGAAACCGCAGGAGAGCTTCAGTCTGAGCGCCCTCCAGCG 547

QY 181 CGGAGCGGAGCAGCCTTCCTGGCTCCAGATCCGACAAAGAGCTTCAGCCATCAGGC 240
Db 546 CGGAGCGGAGCAGCCTTCCTGGCTCCAGATCCGACAAAGAGCTTCAGCCATCAGGC 487

QY 241 CCCACGGAGCTCGCGTGGGCTTCGACCTGGGCAACCCACTACTCTGCTGGGCGCTGT 300
Db 486 CCCACGGAGCTCGCGTGGGCTTCGACCTGGGCAACCCACTACTCTGCTGGGCGCTGT 427

QY 301 TCAGACGGCGCGGTGAGATCTCTGGCCAAACGACCAAGGCAACCGACACACGCCAGCTA 360
Db 426 TCAGACGGCGCGGTGAGATCTCTGGCCAAACGACCAAGGCAACCGACACACGCCAGCTA 367

QY 361 CGTGGCCTTCACCGACACCGAGCGGTGCTGGGGACGCGGCCCAAGAGCGCGCCCT 420
Db 121 AGCCGGCTTCGGCGCAGAGAAACCGCAGGAGAGCTTCAGTCTGAGCGCCCTTCGACCG 180
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RESULT 3

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US-11-266-748A-240242
; Sequence 240242, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 240242
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (187)..(211)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-240242

Query Match 20.8%; Score 519; DB 8; Length 1276;
Best Local Similarity 99.7%; Pred. No. 2.5e-251;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGCGGGCGGGCGGGAGGCTTCGACTGGGGCGGAAGGTTCGGGAAGGTTTCGGCGG 60
Db 551 CCCGGCGGGCGGGCGGGAGGCTTCGACTGGGGCGGAAGGTTCGGGAAGGTTTCGGCGG 610

QY 61 GCGGGGTTCGGGGAGGTGCAAAAGGATGAAAGCCCTGGAAGCGGAGCTGAGCAGATCCG 120
Db 611 GCGGGGTTCGGGGAGGTGCAAAAGGATGAAAGCCCTGGAAGCGGAGCTGAGCAGATCCG 670

QY 121 AGCCGGCTTCGGCGCAGAGAAACCGCAGGAGAGCTTCAGTCTGAGCGCCCTTCGACCG 180
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Mon Nov 6 11:55:56 2006

Db 671 AGCGGGCTGGCGGCGAGAGAAACCGCAGGAGAGCTCACTGCTGAGCGCCCTCGACGG 730
Qy 181 CGGAGCGGCAGCAGCTCCGTGGCCCTCCAGCATCCGACAAAGAGCTTCAGCCATGAGGC 240
Db 731 CGGAGCGGCAGCAGCTCCGTGGCCCTCCAGCATCCGACAAAGAGCTTCAGCCATGAGGC 790
Qy 241 CCCACGGGAGCTCGCGTGGGCGATCGACCTGGGCACCACTACTCTGCTGGTGGCGGTGT 300
Db 791 CCCACGGGAGCTCGCGTGGGCGATCGACCTGGGCACCACTACTCTGCTGGTGGCGGTGT 850
Qy 301 TCAGCAGGCGCGTGGGAGATCTTGGGCAACAGCAGGCGCAACCGCACCGCCAGCTA 360
Db 851 TCAGCAGGCGCGTGGGAGATCTTGGGCAACAGCAGGCGCAACCGCACCGCCAGCTA 910
Qy 361 CGTGGCCCTTCCGACACCGAGCGGCTGGTGGGGAGCGCGGCCAAGCCAGCGGCGCCT 420
Db 911 CGTGGCCCTTCCGACACCGAGCGGCTGGTGGGGAGCGCGGCCAAGCCAGCGGCGCCT 970
Qy 421 GAACCCCAACACCGGCTTGCATGCCAAGCGGCTGATCGGGCGCAAGTTTCGCGGACAC 480
Db 971 GAACCCCAACACCGGCTTGCATGCCAAGCGGCTGATCGGGCGCAAGTTTCGCGGACAC 1030
Qy 481 CACGCTGCAGTCGGACATGAAGCACTGGCCCTTCCAGGTGTGAGCGAGGCGGCAAGCC 540
Db 1031 CACGCTGCAGTCGGACATGAAGCACTGGCCCTTCCAGGTGTGAGCGAGGCGGCAAGCC 1090
Qy 541 CAGGTGGCGTATCTACCGCGGGGAGGAGCAAGCGTTCTACCCCGAGGAGATCTCGTC 600
Db 1091 CAAAGTGGCGGTATCTACCGCGGGGAGGAGCAAGCGTTCTACCCCGAGGAGATCTCGTC 1150
Qy 601 CATGGTGTGAGCAAGATGAA 621
Db 1151 CATGGTGTGAGCAAGATGAA 1171

RESULT 4
US-11-266-748A-100981
; Sequence 100981, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100981
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (61)..(61)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-100981
Query Match 16.0%; Score 400; DB 8; Length 702;
Best Local Similarity 99.6%; Pred. No. 3e-191;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1991 GCGAGAGAGGAGGATGATGAGCATCAGAAGAGGAGCTGGAGCAATCTGTGCGCCCAT 2050
Db 197 GCGAGAGAGGAGGATGATGAGCATCAGAAGAGGAGCTGGAGCAATCTGTGCGCCCAT 256
Qy 2051 CTTCTCCAGGCTCTATCGGGGGCTGTGTCCCTGGGGGAGCAGCAGTTGTAGCGCTCAAGC 2110
Db 257 CTTCTCCAGGCTCTATCGGGGGCTGTGTCCCTGGGGGAGCAGCAGTTGTAGCACTCAAGC 316
Qy 2111 CCACCAGGGGAGCCCGACCGGCCCATCATTTGAGGAGGTTGATTTGAATGGCCCTTCG 2170
Db 317 CCACCAGGGGAGCCCGACCGGCCCATCATTTGAGGAGGTTGATTTGAATGGCCCTTCG 376
Qy 2171 TGATTAAGTCAGCTGTGACTGTGAGGCTATCTATGGGCTTCTAGACTGTCTTCTATGA 2230
Db 377 TGATTAAGTCAGCTGTGACTGTGAGGCTATCTATGGGCTTCTAGACTGTCTTCTATGA 436
Qy 2231 TCCTGCGCTTCAGAGATGAAGGCTTGGGGGGTCTTCCCTCCAAAGCTAGACTTTCTT 2290
Db 437 TCCTGCGCTTCAGAGATGAAGGCTTGGGGGGTCTTCCCTCCAAAGCTAGACTTTCTT 496
Qy 2291 TCAGGATTAAGTCAGAGCTTTTGTGCTTTTGGGGGAGGCGGTTCATCTTCTGCTT 2350
Db 497 CCAGGATTAAGTCAGAGCTTTTGTGCTTTTGGGGGAGGCGGTTCATCTTCTGCTT 556
Qy 2351 CAAATAAAAGTCATTAATTTAATAAACTTGTGGCACTTTAAACATTTGCTTTCACCTA 2410
Db 557 CAAATAAAAGTCATTAATTTAATAAACTTGTGGCACTTTAAACATTTGCTTTCACCTA 616
Qy 2411 TATTTGTGTATTTGTTACTTGTATGATGAATTTGTTATGTAATAATATAGTTATAGA 2470
Db 617 TATTTGTGTATTTGTTACTTGTATGATGAATTTGTTATGTAATAATATAGTTATAGA 676
Qy 2471 CCTAAATAAATTTTAAACTC 2492
Db 677 CCTAAATAAATTTTAAACTC 698
RESULT 5
US-11-266-748A-153792/c
; Sequence 153792, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NAME/KEY: misc_feature

;; PRIOR FILING DATE: 2005-07-18
;; NUMBER OF SEQ ID NOS: 483996
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 153792
;; LENGTH: 702
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: {642}..(642)
;; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-153792

Query Match 16.0%; Score 400; DB 8; Length 702;
Best Local Similarity 99.6%; Pred. No. 3e-191;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGGAGCTGGAGCAATCTGTGCCCCCAT 2050
Db 506 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGGAGCTGGAGCAATCTGTGCCCCCAT 447

QY 2051 CTTCTCAGAGCTCTATGGGGGGCTGTGTCCCTGGGGGAGCAGAGTTGTAGCGCTCAAGC 2110
Db 446 CTTCTCAGAGCTCTATGGGGGGCTGTGTCCCTGGGGGAGCAGAGTTGTAGCGCTCAAGC 387

QY 2111 CCACAGGGGAGCCCCAGCACCCGCCCATCATTTGAGGAGGTTGAATTGAATGGCCCTTCG 2170
Db 386 CCACAGGGGAGCCCCAGCACCCGCCCATCATTTGAGGAGGTTGAATTGAATGGCCCTTCG 327

QY 2171 TGATAAGTCAGCTGTGACTGTAGGCTGTATAGGCGCTTCTAGACTGTCTTCTATGA 2230
Db 326 TGATAAGTCAGCTGTGACTGTAGGCTGTATAGGCGCTTCTAGACTGTCTTCTATGA 267

QY 2231 TCCTGCCCTTCAGAGATGAAGGGCTTCGGGGGGTCTTCCCTCCAAAGCTAGAACTTCTT 2290
Db 266 TCCTGCCCTTCAGAGATGAAGGGCTTCGGGGGGTCTTCCCTCCAAAGCTAGAACTTCTT 207

QY 2291 TCAGAGATAACTGAAGTCTTTTGACTTTTGGGGGAGGGCGGTTCATCCTCTTCTGCTT 2350
Db 206 CCCAGGATAACTGAAGTCTTTTGACTTTTGGGGGAGGGCGGTTCATCCTCTTCTGCTT 147

QY 2351 CAAATAAAGTCATTAATTTATAAAGCTGTGGCACTTTAAACATTTGCTTTACCTA 2410
Db 146 CAAATAAAGTCATTAATTTATAAAGCTGTGGCACTTTAAACATTTGCTTTACCTA 87

QY 2411 TATTTTGTATTTTGTACTGTATGATGAATTTTGTATGTAATATATATATATATAGA 2470
Db 86 TATTTTGTATTTTGTACTGTATGATGAATTTTGTATGTAATATATATATATATAGA 27

QY 2471 CCTAAATAAACTTTTAAAACTC 2492
Db 26 CCTAAATAAACTTTTAAAACTC 5

RESULT 6
US-10-511-937-2830
; Sequence 2830, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946

;; PRIOR FILING DATE: 2003-04-24
;; PRIOR APPLICATION NUMBER: US 10/131,831
;; PRIOR FILING DATE: 2002-04-24
;; PRIOR APPLICATION NUMBER: US 10/325,899
;; PRIOR FILING DATE: 2002-12-20
;; NUMBER OF SEQ ID NOS: 3117
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2830
;; LENGTH: 1932
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-511-937-2830

Query Match 11.4%; Score 283; DB 6; Length 1932;
Best Local Similarity 100.0%; Pred. No. 3.9e-132;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 ATGCAGGCCCCACGGGAGCTCGCGTGGGCATCGACTGGGCACCACTTCTGTCGTG 292
Db 1 ATGCAGGCCCCACGGGAGCTCGCGTGGGCATCGACTGGGCACCACTTCTGTCGTG 60

QY 293 GCGGTGTTTCAGCAGGGCGCGTGGGAGATCCTGGCCAAACGACGAGGGCAACCGCACCG 352
Db 61 GCGGTGTTTCAGCAGGGCGCGTGGGAGATCCTGGCCAAACGACGAGGGCAACCGCACCG 120

QY 353 CCAGCTAGCTGCGCTTCCACGACCCGAGCGCTGTCGGGACGCGCGCAAGAGCCAG 412
Db 121 CCAGCTAGCTGCGCTTCCACGACCCGAGCGCTGTCGGGACGCGCGCAAGAGCCAG 180

QY 413 GCGGCCCTGAACCCCAACACCGGTTCGATGCAAGCGGCTGATCGGGCGCAAGTTTC 472
Db 181 GCGGCCCTGAACCCCAACACCGGTTCGATGCAAGCGGCTGATCGGGCGCAAGTTTC 240

QY 473 GCGGACACCAACCGTTCGAGTCCGACATGAAGCACTGGCCCTTCC 515
Db 241 GCGGACACCAACCGTTCGAGTCCGACATGAAGCACTGGCCCTTCC 283

RESULT 7
US-11-266-748A-358486
; Sequence 358486, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 358486
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo Sapiens

US-11-266-748A-358486

Query Match 9.1%; Score 227; DB 8; Length 777;
Best Local Similarity 100.0%; Pred. No. 7e-104;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2266 TTCCTCCAAAGCTAGAACCTTTCTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGG 2325
Db 551 TTCCTCCAAAGCTAGAACCTTTCTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGG 610
Qy 2326 GAGGCGGTTTCATCTCTCTGCTTCAATATAAAGTCATTAATTTATAAAGCTTGTGT 2385
Db 611 GAGGCGGTTTCATCTCTCTGCTTCAATATAAAGTCATTAATTTATAAAGCTTGTGT 670
Qy 2386 GGCACTTTAAACATGCTTTTACCTATATTTTGTGTAATTTTGTACTTTGTATGATGAAT 2445
Db 671 GGCACTTTAAACATGCTTTTACCTATATTTTGTGTAATTTTGTACTTTGTATGATGAAT 730
Qy 2446 TTGTTATGTAATAATAGTTATAGACCTTAATAAATTTTAAAACTC 2492
Db 731 TTGTTATGTAATAATAGTTATAGACCTTAATAAATTTTAAAACTC 777

RESULT 8

US-11-266-748A-441865/c
; Sequence 441865, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 441865
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo Sapiens

US-11-266-748A-441865

Query Match 9.1%; Score 227; DB 8; Length 777;
Best Local Similarity 100.0%; Pred. No. 7e-104;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2266 TTCCTCCAAAGCTAGAACCTTTCTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGG 2325
Db 227 TTCCTCCAAAGCTAGAACCTTTCTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGG 168
Qy 2326 GAGGCGGTTTCATCTCTCTGCTTCAATATAAAGTCATTAATTTATAAAGCTTGTGT 2385
Db 167 GAGGCGGTTTCATCTCTCTGCTTCAATATAAAGTCATTAATTTATAAAGCTTGTGT 108
Qy 2386 GGCACTTTAAACATGCTTTTACCTATATTTTGTGTAATTTTGTACTTTGTATGATGAAT 2445

107 GGCACCTTAAACATGCTTTTCACCTATATTTTGTGTAATTTTGTACTTTGTATGATGAAT 48

2446 TTGTTATGTAATAATAGTTATAGACCTAAATAAATTTTAAAACTC 2492

47 TTGTTATGTAATAATAGTTATAGACCTAAATAAATTTTAAAACTC 1

RESULT 9

US-10-834-268-4047
; Sequence 4047, Application US/10834268
; Publication No. US20060194211A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Strahs, Andrew
; APPLICANT: Immermann, Fred
; APPLICANT: Slonim, Donna K.
; APPLICANT: Dornier, Andrew J.
; TITLE OF INVENTION: Methods for Prognosis and Treatment of Solid Tumors
; FILE REFERENCE: AM101080L2 (031896-013200)
; CURRENT APPLICATION NUMBER: US/10/834,268
; CURRENT FILING DATE: 2004-04-29
; NUMBER OF SEQ ID NOS: 5315
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4047
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-834-268-4047

Query Match 7.5%; Score 187; DB 6; Length 445;
Best Local Similarity 99.3%; Pred. No. 1.1e-83;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1811 GGCTGAGGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 1870
Db 134 GGCTGAGGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 193
Qy 1871 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGCCCTTAGGGACAAGATTCCTCGAAGAGGA 1930
Db 194 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGCCCTTAGGGACAAGATTCCTCGAAGAGGA 253
Qy 1931 CAGCGCAAAAGTCAAGACAAGTGTGAGGAAGTCTTGGCTGGAGCAAAACAGCT 1990
Db 254 CAGCGCAAAATGCAAGACAAGTGTGCGGAAGTCTTGGCTGGAGCAAAACAGCT 313
Qy 1991 GGCAGAGAAGGAGGATGATGAGCATCAGAAAGAGGAGCTGGAGCAAAATCTGTCGCCCAT 2050
Db 314 GGCAGAGAAGGAGGATGATGAGCATCAGAAAGAGGAGCTGGAGCAAAATCTGTCGCCCAT 373
Qy 2051 CTTCTCCAGGCTCTATGCGGGGCTGTGTGTCCTTGGGGGAGCAGTGT 2099
Db 374 CTTCTCCAGGCTCTATGCGGGGCTGTGTGTCCTTGGGGGAGCAGTGT 422

RESULT 10

US-11-266-748A-52935
; Sequence 52935, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03


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; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52935
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-52935

Query Match
Best Local Similarity 7.5%; Score 187; DB 8; Length 518;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1811 GGCTGAGGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 1870
Db 98 GGCTGAGGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 157
Qy 1871 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGGACAAGATTCCCGAAGAGGA 1930
Db 158 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGGACAAGATTCCCGAAGAGGA 217
Qy 1931 CAGCGCAAAAGTCAAGACAGTGTCAAGAGTCTTGGCTGGCTGGAGCACACACAGCT 1990
Db 218 CAGCGCAAAATGCAAGACAGTGTCAAGAGTCTTGGCTGGCTGGAGCACACACAGCT 277
Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 2050
Db 278 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 337
Qy 2051 CTTCTCAGGCTCTATGGGGGCTGTGTGCTGCTGGGGGAGCAGAGTTGT 2099
Db 338 CTTCTCAGGCTCTATGGGGGCTGTGTGCTGCTGGGGGAGCAGAGTTGT 386

RESULT 11
US-11-266-748A-221107
; Sequence 221107, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 221107
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-221107

Query Match
Best Local Similarity 7.5%; Score 187; DB 8; Length 1000;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1811 GGCTGAGGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 1870
Db 333 GGCTGAGGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 392
Qy 1871 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGGACAAGATTCCCGAAGAGGA 1930
Db 393 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGGACAAGATTCCCGAAGAGGA 452
Qy 1931 CAGCGCAAAAGTCAAGACAGTGTCAAGAGTCTTGGCTGGCTGGAGCACACACAGCT 1990
Db 453 CAGCGCAAAATGCAAGACAGTGTCAAGAGTCTTGGCTGGCTGGAGCACACACAGCT 512
Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 2050
Db 513 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 572
Qy 2051 CTTCTCAGGCTCTATGGGGGCTGTGTGCTGCTGGGGGAGCAGAGTTGT 2099
Db 573 CTTCTCAGGCTCTATGGGGGCTGTGTGCTGCTGGGGGAGCAGAGTTGT 621

RESULT 12
US-11-266-748A-395612
; Sequence 395612, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 395612
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-395612
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Query Match 7.5%; Score 187; DB 8; Length 1000;
Best Local Similarity 99.3%; Pred. No. 1.1e-83;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GGCTGAGGATGAGCCCGAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 1870
DB 333 GGCTGAGGATGAGCCCGAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 392

QY 1871 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAGCCTTAGGGAACAAGATTCCCGAAGAGGA 1930
DB 393 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAGCCTTAGGGAACAAGATTCCCGAAGAGGA 452

QY 1931 CAGGCGCAAGTCAAGCAAGTGTCAAGAGTCTTGGCTGGCTGGAGCAACAACAGCT 1990
DB 453 CAGGCGCAAGTCAAGCAAGTGTCAAGAGTCTTGGCTGGCTGGAGCAACAACAGCT 512

QY 1991 GGCAGAGAGGAGGATGAGCATCAGAGAGGAGCTGGAGCAAACTCTGCGCCCAT 2050
DB 513 GGCAGAGAGGAGGATGAGCATCAGAGAGGAGCTGGAGCAAACTCTGCGCCCAT 572

QY 2051 CTTCTCCAGGCTCTATGGGGGCTGGTGTCCCTGGGGGAGCAGTTGT 2099
DB 573 CTTCTCCAGGCTCTATGGGGGCTGGTGTCCCTGGGGGAGCAGTTGT 621

RESULT 13
US-11-266-748A-466658/c
; Sequence 466658, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 466658
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-466658

Query Match 7.5%; Score 187; DB 8; Length 1000;
Best Local Similarity 99.3%; Pred. No. 1.1e-83;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GGCTGAGGATGAGCCCGAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 1870
DB 668 GGCTGAGGATGAGCCCGAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 609

QY 1871 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAGCCTTAGGGAACAAGATTCCCGAAGAGGA 1930
DB 608 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAGCCTTAGGGAACAAGATTCCCGAAGAGGA 549

QY 1931 CAGGCGCAAGTCAAGCAAGTGTCAAGAGTCTTGGCTGGCTGGAGCAACAACAGCT 1990
DB 548 CAGGCGCAAAATGCAAGCAAGTGTTCGGGAAGTCTTGGCTGGCTGGAGCAACAACAGCT 489

QY 1991 GGCAGAGAGGAGGATGATGAGCATCAGAGAGGAGCTGGAGCAAACTCTGCGCCCAT 2050
DB 488 GGCAGAGAGGAGGATGATGAGCATCAGAGAGGAGCTGGAGCAAACTCTGCGCCCAT 429

QY 2051 CTTCTCCAGGCTCTATGGGGGCTGGTGTCCCTGGGGGAGCAGTTGT 2099
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RESULT 14
US-11-266-748A-13932
; Sequence 13932, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13932
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-13932

Query Match 6.7%; Score 167; DB 8; Length 559;
Best Local Similarity 99.3%; Pred. No. 1.4e-73;
Matches 267; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1831 GGCACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGTCTCCATGTGAAGGTTCTT 1890
DB 5 GGCACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGTCTCCATGTGAAGGTTCTT 64

QY 1891 TGCAAGAGGAAGCCTTAGGGACAAGATTCCCAAGAGGACAGCGCAAAAGTGCAAGACA 1950
DB 65 TGCAAGAGGAAGCCTTAGGGACAAGATTCCCAAGAGGACAGCGCAAAATGCAAGACA 124

QY 1951 AGTGTCAAGAGTCTTGGCTGGAGCAACAACAGCTGGCAGAGAGGAGGATATG 2010
DB 125 AGTGTGGGAAGTCTTGGCTGGAGCAACAACAGCTGGCAGAGAGGAGGATATG 184

QY 2011 AGCATCAGAGAGGAGCTGGAGCAAACTCTGCGCCCATCTTCTCCAGGCTCTATGGGG 2070
DB 185 AGCATCAGAGAGGAGCTGGAGCAAACTCTGCGCCCATCTTCTCCAGGCTCTATGGGG 244

QY 2071 GGCCTGGTGTCCCTGGGGGAGCAGTTGT 2099

Db 245 GGCCTGGTGTCCCTGGGGGACAGAGTTGT 273

RESULT 15

US-11-266-748A-56036
; Sequence 56036, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56036
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-56036

Query Match 5.7%; Score 143; DB 8; Length 682;
Best Local Similarity 99.2%; Pred. No. 1.8e-61;
Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1811 GGCTGAGGATCAGGCCAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 1870
Db 109 GGCTGAGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 168
Qy 1871 CTTCCATGTGAAAGTTCTTTGCAAGAGGAAAGCCTTAGGGAACAAGATCCCGAAGAGGA 1930
Db 169 CTTCCATGTGAAAGTTCTTTGCAAGAGGAAAGCCTTAGGGAACAAGATCCCGAAGAGGA 228
Qy 1931 CAGGCGCAAGTGCAGACAAGTGTACGGAAGTCTTGCTGGCTGGAGCACAACAGCT 1990
Db 229 CAGGCGCAAAATGCAAGACAAGTGTTCGGGAAGTCTTGCTGGCTGGAGCACAACAGCT 288
Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAAAGAGGAGCTGGAGCAAAATCTGTCGCCCAT 2050
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Db 349 CTTCT 353

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Job time : 523.48 secs

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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	587	23.5	698	7	BF448220
C 6	582	23.3	676	4	CA426117
C 7	579	23.2	579	4	CA391777
C 8	564	22.6	1003	4	EX357704
C 9	535	21.5	537	1	AI652340
C 10	534	21.4	534	7	BF590626
C 11	512	20.5	567	9	DB017526
C 12	508	20.4	662	9	DA828714
C 13	503	20.2	852	3	BQ212261
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23	495	19.9	582	9	DB204579
24	495	19.9	583	3	BP208756
25	495	19.9	584	9	DB170275
26	495	19.9	589	9	DA389790
27	495	19.9	590	9	DA593582
28	495	19.9	600	9	DA941037
29	495	19.9	1056	2	BM546945
30	495	19.9	2878	6	CR623806
31	494	19.8	565	9	DB103143
32	493	19.8	564	9	DA594610
33	491	19.7	562	9	DA010341
34	490	19.7	561	9	DA592862
35	490	19.7	561	9	DB013313
36	486	19.5	591	9	DB200528
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38	476	19.1	547	9	DB127250
39	473	19.0	544	9	DB102455
40	472	18.9	543	9	DA963272
41	468	18.8	591	9	DB202792
42	467	18.7	518	9	DB208890
C 43	467	18.7	531	9	DB328896
44	467	18.7	538	9	DB117002
45	463	18.6	534	9	DA961155

ALIGNMENTS

BM677874 764 bp mRNA linear EST 27-FEB-2002
UI-E-EJ0-aie-1-08-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-aie-1-08-0-UI 3', mRNA sequence.
ACCESSION BM677874
VERSION BM677874.1 GI:18987770
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 764)
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa, 4156 MEBRF, Iowa City, IA 52242, USA
375 Newton Road,
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=yes.
FEATURES
Location/Qualifiers
1..764
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-aie-1-08-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and

Choroid"
/dev_stage="fetal and adult"
/lab_host="PH10B (Life Technologies) (T1 phase resistant)"
/clone_lib="UI-E-EJ0"
/notes="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ0 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAAGA; lens, CGATTAGGA; eye anterior segment, AATCCGCAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG_TISSUE=human lens TAG_LIB=UI-E-EJ0 TAG_SEQ=CGATTAGCGA"

ORIGIN		Query Match	26.5%;	Score 660;	DB 3;	Length 764;		
		Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1833	GACAGAGTGGTCCGCAAAACCTCGCTGGAGGCCATCTCTCCATGTGAAGTCTTTG	1892					
Db	678	GACAGAGTGGTCCGCAAAACCTCGCTGGAGGCCATCTCTCCATGTGAAGTCTTTG	619					
QY	1893	CAAGAGAAAGCTTAGGACAAAGATTCGGAAGGACGCGCAAGTCCAGACAAG	1952					
Db	618	CAAGAGAAAGCTTAGGACAAAGATTCGGAAGGACGCGCAAGTCCAGACAAG	559					
QY	1953	TGTCAGAAAGTCTTCCCTGGCTGGAGCAACACCACTGGCAGAGAGGAGATGAG	2012					
Db	558	TGTCAGAAAGTCTTCCCTGGCTGGAGCAACACCACTGGCAGAGAGGAGATGAG	499					
QY	2013	CATCAGAGAGGAGCTGGAGCAAACTGTGCGCCCATCTCTCCAGGCTCTATGGGGG	2072					
Db	498	CATCAGAGAGGAGCTGGAGCAAACTGTGCGCCCATCTCTCCAGGCTCTATGGGGG	439					
QY	2073	CCTGGTGTCTGGGGGCGAGTTGATGAAATGGCCCTTCTGATAGTCAAGTCACTGTC	2132					
Db	438	CCTGGTGTCTGGGGGCGAGTTGATGAAATGGCCCTTCTGATAGTCAAGTCACTGTC	379					
QY	2133	GGCCCCCATCATGAGGAGGTTGATGAAATGGCCCTTCTGATAGTCAAGTCACTGTC	2192					
Db	378	GGCCCCCATCATGAGGAGGTTGATGAAATGGCCCTTCTGATAGTCAAGTCACTGTC	319					
QY	2193	AGGGCTATGCTATGGCCCTTCTAGACTCTCTCTATGATCTCTGCTTCCAGATGAAGG	2252					
Db	318	AGGGCTATGCTATGGCCCTTCTAGACTCTCTCTATGATCTCTGCTTCCAGATGAAGG	259					
QY	2253	GCTTGGGGGGGTCTTCCCTCCAAAGCTAGAACTTCTTCCAGATGAAGTCTTTT	2312					
Db	258	GCTTGGGGGGGTCTTCCCTCCAAAGCTAGAACTTCTTCCAGATGAAGTCTTTT	199					
QY	2313	GACTTTTGGGGGGGGGGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2372					
Db	198	GACTTTTGGGGGGGGGGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	139					
QY	2373	TTAAAACTTGTGTGGCACTTTAACTGCTTTCACCTATATTTTGTGTTTACTT	2432					
Db	138	TTAAAACTTGTGTGGCACTTTAACTGCTTTCACCTATATTTTGTGTTTACTT	79					
QY	2433	GTATGTATGAAATTTTGTATGTAATAATATAGTTATAGACTAAATAAATCTT	2492					
Db	78	GTATGTATGAAATTTTGTATGTAATAATATAGTTATAGACTAAATAAATCTT	19					

RESULT 2
BU617655/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

707 bp mRNA linear EST 23-SEP-2002
UI-H-DF0-beq-b-22-0-UI-s1 NCI CGAP DF0 Homo sapiens cDNA clone
UI-H-DF0-beq-b-22-0-UI 3', mRNA sequence.
BU617655
BU617655.1 GI:23283870
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 707)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Jose Marcuende
cDNA Library Prepared by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

Location/Qualifiers
1..707
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-beq-b-22-0-UI"
/tissue_type="Subchondral Bone"
/stage="Adult"
/lab_host="PH10B (Life Technologies)"
/clone_lib="NCI-CGAP DF0"
/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.
TAG_LIB=UI-H-DF0
TAG_TISSUE=subchondral bone
TAG_SEQ=GTTAAGCGTC"

ORIGIN

		Query Match	26.4%;	Score 659;	DB 3;	Length 707;		
		Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1834	ACAGAGTGGTCCGCAAAACCTCGCTGGAGGCCATCTCTCCATGTGAAGTCTTTG	1893					
Db	677	ACAGAGTGGTCCGCAAAACCTCGCTGGAGGCCATCTCTCCATGTGAAGTCTTTG	618					
QY	1894	AGAGGAAAGCTTAGGACAAAGATTCGGAAGGACGAGCGCAAGTCCAGACAAGT	1953					
Db	617	AGAGGAAAGCTTAGGACAAAGATTCGGAAGGACGAGCGCAAGTCCAGACAAGT	558					
QY	1954	GTGAGAAAGTCTTCCCTGGCTGGAGCAACACCTGCGCAGAGAGGAGATGAGC	2013					
Db	557	GTGAGAAAGTCTTCCCTGGCTGGAGCAACACCTGCGCAGAGAGGAGATGAGC	498					

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QY 2014 ATCAGAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCAGGCTCTATGGGGGC 2073
Db 497 ATCAGAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCAGGCTCTATGGGGGC 438
QY 2074 CTGGTGTCCTGGGGGAGCAGTGTAGCGTCAAGCCACACAGGGGAGCCACGACCG 2133
Db 437 CTGGTGTCCTGGGGGAGCAGTGTAGCGTCAAGCCACACAGGGGAGCCACGACCG 378
QY 2134 GCCCATCATTTAGGAGGTTGATTGAATGCGCTTCTGTATAGTCAAGTGTGACTGTCA 2193
Db 377 GCCCATCATTTAGGAGGTTGATTGAATGCGCTTCTGTATAGTCAAGTGTGACTGTCA 318
QY 2194 GGGCTATGCTATGGGCTTCTAGACTCTTCTATGATCTCTGCTTCCCTTTAGAGATGAAGG 2253
Db 317 GGGCTATGCTATGGGCTTCTAGACTCTTCTATGATCTCTGCTTCCCTTTAGAGATGAAGG 258
QY 2254 CTGGGGGGCTTCCCTCCAAAGCTAGAACTTCTTCCAGATTAAGTCTTTTGG 2313
Db 257 CTGGGGGGGCTTCCCTCCAAAGCTAGAACTTCTTCCAGATTAAGTCTTTTGG 198
QY 2314 ACTTTTGGGGGAGGCGGTTCATCTCTTCTGCTTCAATAAAAGTCAATTAATAT 2373
Db 197 ACTTTTGGGGGAGGCGGTTCATCTCTTCTGCTTCAATAAAAGTCAATTAATAT 138
QY 2374 TAAACTTGTGTGGCACTTTAAACATGCTTTCACCTATATTTTGTGTAATTTGTTACTTG 2433
Db 137 TAAACTTGTGTGGCACTTTAAACATGCTTTCACCTATATTTTGTGTAATTTGTTACTTG 78
QY 2434 TATGTATGAATTTTGTATGTAATATATGTTATAGACCTTAAATTAACCTTTTAAACTC 19
Db 77 TATGTATGAATTTTGTATGTAATATATGTTATAGACCTTAAATTAACCTTTTAAACTC 19
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RESULT 3

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B0918107
LOCUS B0918107 936 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT 8822790 Lupski sciatic nerve Homo sapiens cDNA clone
IMAGE:6203181 5', mRNA sequence.
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B0918107

B0918107.1 GI:22332805

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 936)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM13622 row: g column: 22

High quality sequence stop: 650.

Location/Qualifiers

1. .936

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6203181"

/sex="male"

/tissue_type="sciatic nerve"

/dev_stage="adult, 70 yr"

/lab_host="DH10B"

/clone_lib="Lupski_sciatic_nerve"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCACGCTCCG-3' and
5'-GACTATTTCTAGATCCGAGCGCCCTT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupeki, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

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Query Match 25.4%; Score 632; DB 3; Length 936;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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Db 1 GCGCGTTTGGAGAACTGTCTCAGACCTTCTCCGAGACACCTTGAGCGGTGGAGAAG 60  
  
QY 1196 GCGCTCGCGGATGCCAAGCTGGACAAAGGCCAGATTTCATGACTTCCTGCTGGGGGAGGG 1255  
Db 61 GCGCTCGCGGATGCCAAGCTGGACAAAGGCCAGATTTCATGACTTCCTGCTGGGGGAGGG 120  
  
QY 1256 CTCACCTCGCATCCCCAAGGTGACAAAGTTGCTGCAAGGACTTCTTCAACGCGCAAGAGCT 1315  
Db 121 CTCACCTCGCATCCCCAAGGTGACAAAGTTGCTGCAAGGACTTCTTCAACGCGCAAGAGCT 180  
  
QY 1316 GAACAAGACATCAACCTTGATGAGGCTGTGCGCTATGGGTCTGTGTCAGCGCGCGCT 1375  
Db 181 GAACAAGACATCAACCTTGATGAGGCTGTGCGCTATGGGGCTGTGTCAGCGCGCGCT 240  
  
QY 1376 GTTGATGGGGGACAAATGTGAGAAAGTGCAGATCTCTGCTGCTGCGAGTGCCTCCCT 1435  
Db 241 GTTGATGGGGGACAAATGTGAGAAAGTGCAGATCTCTGCTGCTGCGAGTGCCTCCCT 300  
  
QY 1436 GTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGACACCGCTGATCCAGAGGAACGCCAC 1495  
Db 301 GTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGACACCGCTGATCCAGAGGAACGCCAC 360  
  
QY 1496 TATCCCGACCAAGCAGACCCAGACTTTTCAACCTTACTCGGACACAGCTGGGGTCTTT 1555  
Db 361 TATCCCGACCAAGCAGACCCAGACTTTTCAACCTTACTCGGACACAGCTGGGGTCTTT 420  
  
QY 1556 CATCCAGGTGTATGAGTTTGAGAGGCGCATGACCAAGGACCAACCTCTCTGGGGCGTTT 1615  
Db 421 CATCCAGGTGTATGAGTTTGAGAGGCGCATGACCAAGGACCAACCTCTCTGGGGCGTTT 480  
  
QY 1616 TGAACCTATTGGCATCCCTCTCTGCCCCCAGATGGAGTCCCCCAGATAGAGTGCAGTTTGA 1675  
Db 481 TGAACCTATTGGCATCCCTCTCTGCCCCCAGATGGAGTCCCCCAGATAGAGTGCAGTTTGA 540  
  
QY 1676 CATTCATGCTAATGGCATCTCTGAGCGTGCAGCCACTGACAGGACACAGGTAAGGCTAA 1735  
Db 541 CATTCATGCTAATGGCATCTCTGAGCGTGCAGCCACTGACAGGACACAGGTAAGGCTAA 600  
  
QY 1736 CAAGATCAACATGACAGGCGCGTGCAGCAAGGAGGAGGAGGATGCTTCATCA 1795  
Db 601 CAAGATCAACATGACAGGCGCGTGCAGCAAGGAGGAGGAGGATGCTTCATCA 660  
  
QY 1796 AGCCGAGCAGTACGGGGCTGAGGATGAGGCCACAGAGGACAGATGGTGCACAAAATCTC 1855  
Db 661 AGCCGAGCAGTACGGGGCTGAGGATGAGGCCACAGAGGACAGATGGTGCACAAAATCTC 720  
  
QY 1856 GCTGAGGCCCATG 1869  
Db 721 GCTGAGGCCCATG 734
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RESULT 4

DR004990

LOCUS

DEFINITION

TC118784 Human placenta, large insert, pCMV expression library Homo

sapiens

EST 17-MAY-2005

linear

mRNA

709 bp

pCMV expression library Homo

the normalized library NCI_CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN		FEATURES		POLYA=Yes		
Query Match		Location/Qualifiers				
Best Local Similarity		1. .676				
Matches	587; Conservative	0; Mismatches		0; Indels	0; Gaps	
0; Indels		0; Gaps				
Qy	1906	TTAGGGACAAGATTCCGAAGAGGACAGGGCGCAAGTGCAAGCAAAAGTGTGAGGAGTCC	1965			
Db	591	TTAGGGACAAGATTCCGAAGAGGACAGGGCGCAAGTGCAAGCAAAAGTGTGAGGAGTCC	532			
Qy	1966	TTGGCTGGTGGAGCACACAGCTGGCAGAGAGGAGGATGAGCATCAGAAGAGGG	2025			
Db	531	TTGGCTGGTGGAGCACACAGCTGGCAGAGAGGAGGATGAGCATCAGAAGAGGG	472			
Qy	2026	AGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTGTGTCCTCG	2085			
Db	471	AGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTGTGTCCTCG	412			
Qy	2086	GGGGCAGCAGTGTGAGCGCTCAAGCCACAGGGGGGACCCAGCACCGGCGCCCATCATTTG	2145			
Db	411	GGGGCAGCAGTGTGAGCGCTCAAGCCACAGGGGGGACCCAGCACCGGCGCCCATCATTTG	352			
Qy	2146	AGGAGGTTGATGAATGGCCCTTCGTGATGAAGTCAGCTGTGACTGTGAGGGCTATGCTAT	2205			
Db	351	AGGAGGTTGATGAATGGCCCTTCGTGATGAAGTCAGCTGTGACTGTGAGGGCTATGCTAT	292			
Qy	2206	GGGGCTTCTAGACTGTCTCTATGATCCTGCCTTCAGAGATGAAGGCTTGGGGGGTTC	2265			
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Qy	2326	GAGGGGGTTCATCTCTCTGCTTCAATATAAAGTCATTAATTTATTAACCTTGTGT	2385			
Db	171	GAGGGGGTTCATCTCTCTGCTTCAATATAAAGTCATTAATTTATTAACCTTGTGT	112			
Qy	2386	GGCACTTTAACTTGTCTTCACTATATTTTGTGATTTTGTACTTGTATGATGAATT	2445			
Db	111	GGCACTTTAACTTGTCTTCACTATATTTTGTGATTTTGTACTTGTATGATGAATT	52			
Qy	2446	TTGTTATGTAATAATATAGTTATAGACCTAAATAAATTTTAAACTC	2492			
Db	51	TTGTTATGTAATAATATAGTTATAGACCTAAATAAATTTTAAACTC	5			
RESULT 6						
CA426117/c						
LOCUS						
DEFINITION						
UI-H-DF0-bek-o-20-0-UI.s1 NCI CGAP_DF0 Homo sapiens cDNA clone						
UI-H-DF0-bek-o-20-0-UI.3', mRNA sequence.						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
Homo sapiens (human)						
Homo sapiens						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;						
Hominidae; Homo.						
REFERENCE						
AUTHORS						
TITLE						
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.						
JOURNAL						
Unpublished (1997)						
COMMENT						
Contact: Robert Strausberg, Ph.D.						

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD

FEATURES

Location/Qualifiers

1. .676

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

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/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP_DF0"

/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dtr)18 tail. The sequence tag for this library is GTTAAGCGTC.

TAG_ISSUE=Subchondral bone

TAG_LIB=UI-H-DF0

TAG_SEQ=GTTAAGCGTC

ORIGIN

Query Match 23.3%; Score 582; DB 4; Length 676;

Best Local Similarity 100.0%; Pred. No. 2.5e-297;

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1911 GACAAATGTCGCGCCCATCTTCCAGGCTCTATGGGGGCTGTGCTCCCTGGGGG 2090

Db 600 GACAAATGTCGCGCCCATCTTCCAGGCTCTATGGGGGCTGTGCTCCCTGGGGG 421

Qy 1971 TGGCTGGAGCAACCCAGCTGCGAGAGAGGAGGATGAGCATCAGAAGAGGAGCTG 2030

Db 540 TGGCTGGAGCAACCCAGCTGCGAGAGAGGAGGATGAGCATCAGAAGAGGAGCTG 481

Qy 2031 GAGCAAAATGTCGCGCCCATCTTCCAGGCTCTATGGGGGCTGTGCTCCCTGGGGG 2090

Db 480 GAGCAAAATGTCGCGCCCATCTTCCAGGCTCTATGGGGGCTGTGCTCCCTGGGGG 421

Qy 2091 AGCAGTTGTAGCGCTCAAGCCCAAGGGGGAGAGGAGGAGGAGGAGGAGGAG 2150

Db 420 AGCAGTTGTAGCGCTCAAGCCCAAGGGGGAGAGGAGGAGGAGGAGGAGGAG 361

Qy 2151 GTTGATTGAATGGCCCTTCTGATGAAGTCAGCTGTGACTGTGAGGGCTATGCTATGGGG 2210

Db 360 GTTGATTGAATGGCCCTTCTGATGAAGTCAGCTGTGACTGTGAGGGCTATGCTATGGGG 301

Qy 2211 TTCTAGACTGTCTCTATGATGCTCCCTTTCAGAGATGAAGGGCTTGGGGGGGCTCTTCCC 2270

Db 300 TTCTAGACTGTCTCTATGATGCTCCCTTTCAGAGATGAAGGGCTTGGGGGGGCTCTTCCC 241

Qy 2271 TCCAAAGCTAGAACTTTCTTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGGGAGGG 2330

Db 240 TCCAAAGCTAGAACTTTCTTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGGGAGGG 181

Qy 2331 CGGTTATCTCTCTCTGCTTCAAAATAAAGTCATTAATTTATTAACCTTGTGTGGGAC 2390

Db 180 CGGTTATCTCTCTCTGCTTCAAAATAAAGTCATTAATTTATTAACCTTGTGTGGGAC 121

Mon Nov 6 11:55:56 2006

QY	2391	TTTAACTAGCTTTACCTATATTTTGTGTATTTTGTACTTGTATGATGAATTTTGT	2450
Db	120	TTTAACTAGCTTTACCTATATTTTGTGTATTTTGTACTTGTATGATGAATTTTGT	61
QY	2451	ATGTAAATATAGTTATAGACCTTAATAAATTTTAAATCT	2492
Db	60	ATGTAAATATAGTTATAGACCTTAATAAATTTTAAATCT	19
RESULT 7			
CA391777			
LOCUS	579 bp	mRNA	linear
DEFINITION	cs18905.y1 Human Retinal pigment epithelium/choroid cDNA		EST 06-NOV-2002
SOURCE	(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs18905		
ACCESSION	CA391777		
VERSION	CA391777.1	GI:24723954	
KEYWORDS	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Wislow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.		
TITLE	Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants		
JOURNAL	Mol. Vis. 8 (4), 205-220 (2002)		
PUBMED	12107410		
COMMENT	Contact: Wistow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 18 row: g column: 05 Seq primer: M13RPI reverse primer (ABI). Location/Qualifiers 1. .579 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="cs18905" /tissue_type="RPE/choroid" /dev_stage="Adult" /lab_host="EMDH10B" /clone_lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs" /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."		
FEATURES			
source			
ORIGIN			
Query Match	23.2%	Score 579;	DB 4; Length 579;
Best Local Similarity	100.0%	Pred. No. 9.9e-296;	
Matches 579;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	690	GTAACCTCGCAGCGCAGGCGCACCAAGGACGCGGGGGCCATCGCGGGCTCAAGGTGTGC	749
Db	1	GTAACCTCGCAGCGCAGGCGCACCAAGGACGCGGGGGCCATCGCGGGCTCAAGGTGTGC	60
QY	750	CGATCATCAATGAGCGCACCGCAGCGCATGCTATGGGCTGACCGCGGGCGCGG	809
Db	61	CGATCATCAATGAGCGCACCGCAGCGCATGCTATGGGCTGACCGCGGGCGCGG	120
QY	810	GAAGCGCAACGTGCTCATTTTGGACCTGGGTGGGGGACCTTTCGATGTGCGTTCTCT	869
Db	121	GAAGCGCAACGTGCTCATTTTGGACCTGGGTGGGGGACCTTTCGATGTGCGTTCTCT	180
QY	870	CCATTGACGCGCGGTGTCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAG	929
Db	181	CCATTGACGCGCGGTGTCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAG	240
QY	930	AGGACTTCGACCAACCGGCTCGTGAACCACTTTCATGAAGAATTCGCGGCGGAACATGGGA	989
Db	241	AGGACTTCGACCAACCGGCTCGTGAACCACTTTCATGAAGAATTCGCGGCGGAACATGGGA	300
QY	990	AGGACTTCGAGCGGGAACAAGCGTGCCTGCGCAGGCTGGCAGCTGTGAGCGCGCCA	1049
Db	301	AGGACTTCGAGCGGGAACAAGCGTGCCTGCGCAGGCTGGCAGCTGTGAGCGCGCCA	360
QY	1050	AGCGACCCCGTCTCCAGCACCCAGCCACCTGGAGATAGACTCCCTGTTTCGAGGGCG	1109
Db	361	AGCGACCCCGTCTCCAGCACCCAGCCACCTGGAGATAGACTCCCTGTTTCGAGGGCG	420
QY	1110	TGGACTTCTACAAGTCCATCACTCGTCCCGCTTTGAGGAACCTGTGCTCAGACTCTTCC	1169
Db	421	TGGACTTCTACAAGTCCATCACTCGTCCCGCTTTGAGGAACCTGTGCTCAGACTCTTCC	480
QY	1170	GCAGCACCTTGAGCGCGTGGAGAGCCCTGCGGGATGCCAAGCTGGACAAGGCCCAGA	1229
Db	481	GCAGCACCTTGAGCGCGTGGAGAGCCCTGCGGGATGCCAAGCTGGACAAGGCCCAGA	540
QY	1230	TTTCATGACTTCGCTCTGGGGGAGGGCTCCACTCGCATC	1268
Db	541	TTTCATGACTTCGCTCTGGGGGAGGGCTCCACTCGCATC	579
RESULT 8			
LOCUS	1003 bp	mRNA	linear
DEFINITION	EST. Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI029VJ23 3-PRIME, mRNA sequence.		
ACCESSION	BX357704		
VERSION	BX357704.2	GI:46289402	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1003)		
JOURNAL	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.		
COMMENT	Full-length cDNA libraries and normalization Unpublished (2001) On May 5, 2003 this sequence version replaced gi:30370149. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1112.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?se=CS0DI029CE12NP1&c=1112.f.		
FEATURES			
source			
Location/Qualifiers			
1. .1003			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			

QY	1839	GTGGCTGCCAAAACTCGCTGGAGGCCCATGCTTCCATGTGAAAGTCTTTTGCAGAG	1898
Db	534	GTGGCTGCCAAAACTCGCTGGAGGCCCATGCTTCCATGTGAAAGTCTTTTGCAGAG	475
QY	1899	GAAGCCTTAGGACCAAGATTCCCGAAGGACAGCGGCAAGTGCAGCAAGTCTCAG	1958
Db	474	GAAGCCTTAGGACCAAGATTCCCGAAGGACAGCGGCAAGTGCAGCAAGTCTCAG	415
QY	1959	GAATCTCTGCTGGCTGGAGCAACACCGCTGCAGAGAGGAGGATGATGAGCATCAG	2018
Db	414	GAATCTCTGCTGGCTGGAGCAACACCGCTGCAGAGAGGAGGATGATGAGCATCAG	355
QY	2019	AAGAGGAGCTGGAGCAAACTCTGCGCCCATCTTCCAGGCTCTATGGGGGCTGGT	2078
Db	354	AAGAGGAGCTGGAGCAAACTCTGCGCCCATCTTCCAGGCTCTATGGGGGCTGGT	295
QY	2079	GTCCCTGGGGGACAGCTTGTAGCGCTCAAGCCACAGGGGACCCAGCAGCGGCC	2138
Db	294	GTCCCTGGGGGACAGCTTGTAGCGCTCAAGCCACAGGGGACCCAGCAGCGGCC	235
QY	2139	ATCATTTAGGAGCTTGTGAATGCGCTTCGTGATAAGTCAGCTGTGACGTCTGAGGCT	2198
Db	234	ATCATTTAGGAGCTTGTGAATGCGCTTCGTGATAAGTCAGCTGTGACGTCTGAGGCT	175
QY	2199	ATGCTATGGGCTTCTAGACTGTCTTATGATCTGCTCCCTTCAGAGATGAAGGCTGG	2258
Db	174	ATGCTATGGGCTTCTAGACTGTCTTATGATCTGCTCCCTTCAGAGATGAAGGCTGG	115
QY	2259	GGGGCTCTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAACTCTTTGACTTT	2318
Db	114	GGGGCTCTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAACTCTTTGACTTT	55
QY	2319	TTGGGGGAGGGCGGTTCATCTCTCTGCTTCAATTAATAAGTCAATTAATTA	2372
Db	54	TTGGGGGAGGGCGGTTCATCTCTCTGCTTCAATTAATAAGTCAATTAATTA	1
RESULT 11			
DB017526			
LOCUS	DB017526	TESOP2 Homo sapiens cDNA clone TESOP2007084 5', mRNA	linear EST 13-NOV-2005
DEFINITION	DB017526	sequence.	
ACCESSION	DB017526	GI:82361027	
VERSION	DB017526.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 567)		
AUTHORS	Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.		
TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes		
JOURNAL	Genome Res. 16 (1), 55-65 (2006)		
PUBMED	16344560		
COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology		

QY	2258	GGGGGCTTTCCCTCCAAAGCTAGAACTTTTTCAGGATAACTGAACTCTTTGACTT	2317
Db	237	GGGGGCTTTCCCTCCAAAGCTAGAACTTTTTCAGGATAACTGAACTCTTTGACTT	178
QY	2318	TTTGGGGGAGGGGCTTCATCTCTGCTTCAAAATAAAAAAGTCATTAATTAATAA	2377
Db	177	TTTGGGGGAGGGGCTTCATCTCTGCTTCAAAATAAAAAAGTCATTAATTAATAA	118
QY	2378	ACTTGTGTGGCAGCTTTAAACATCTGCTTACCTATATTTTGTGTATTTTGTACTGTATG	2437
Db	117	ACTTGTGTGGCAGCTTTAAACATCTGCTTACCTATATTTTGTGTATTTTGTACTGTATG	58
QY	2438	TATGAATTTTGTATGTAATAATAGTTATAGACCTAAATAAACTTTTAAACCTC	2492
Db	57	TATGAATTTTGTATGTAATAATAGTTATAGACCTAAATAAACTTTTAAACCTC	3

RESULT 10			
BF590626/c			
LOCUS	BF590626	534 bp mRNA linear EST 12-DEC-2000	
DEFINITION	7h40h11.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:3318501 3', similar to SW:HS76_HUMAN P17066 HEAT SHOCK 70 KD PROTEIN 6 ;, mRNA sequence.		
ACCESSION	BF590626		
VERSION	BF590626.1	GI:11683037	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 534)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: info@image.llnl.gov Seq primer: -40UP from Gibco High quality sequence stop: 474.		
FEATURES	Location/Qualifiers		
source	1..534		
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	/clone="IMAGE:3318501"		
	/tissue_type="colon tumor, RER+"		
	/lab_host="DH10B"		
	/clone_lib="NCI CGAP Col6"		
	/note="Organ: colon; Vector: pT7T3D-PacI; Site 1; Not I; Site 2; Eco RI; Plasmid DNA from the normalized library NCI CGAP Col6 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneID# 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo."		

ORIGIN			
Query Match	21.4%	Score 534; DB 7; Length 534;	
Best Local Similarity	100.0%; Pred. No. 8.8e-272;		
Matches 534; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		

Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

source
Location/Qualifiers
1..567
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TESOP2007084"
/tissue_type="esophageal, tumor tissue"
/clone_lib="TESOP2"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 20.5%; Score 512; DB 9; Length 567;
Best Local Similarity 99.8%; Pred. No. 4.6e-260;
Matches 562; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 114 AGATCCGAGCGGCTGGCGGACAGAAACCGCAGGAGAGCTCACTGTGAGCGCCCC 173
Db |||||
5 AGATCCGAGCGGCTGGCGGACAGAAACCGCAGGAGAGCTCACTGTGAGCGCCCC 64
QY 174 TCGACGGCGGACGGCAGCAGCTCCGTGGCTCCAGCATCCGACAAAGAGCTTCAGCCA 233
Db |||||
65 TCGACGGCGGAGCGGAGCAGCTCCGTGGCTCCAGCATCCGACAAAGAGCTTCAGCCA 124
QY 234 TCGAGGCCCCACGGGAGCTCGCGTGGGCATCGACTGGGCACCACCTACTCTGTCGTGG 293
Db |||||
125 TCGAGGCCCCACGGGAGCTCGCGTGGGCATCGACTGGGCACCACCTACTCTGTCGTGG 184
QY 294 GCGTGTTCAGCAGCGGCGGTGAGATCTCTGGCACAACGACCGAGGCAACCGCACACGC 353
Db |||||
185 GCGTGTTCAGCAGCGGCGGTGAGATCTCTGGCACAACGACCGAGGCAACCGCACACGC 244
QY 354 CCAGCTACGTGGCTTCACGACACCGAGCGGCTGTGGGAGCGCGGCCCAAGGCCAGG 413
Db |||||
245 CCAGCTACGTGGCTTCACGACACCGAGCGGCTGTGGGAGCGCGGCCCAAGGCCAGG 304
QY 414 CGGCCCTGAACCCCCACAACACCGTGTTCGATGCAAGCGGCTGATCGGCGCAAGTTCC 473
Db |||||
305 CGGCCCTGAACCCCCACAACACCGTGTTCGATGCAAGCGGCTGATCGGCGCAAGTTCC 364
QY 474 CGGACACACGCTGAGTCGACATGAAGCACTGGCCCTTCAGAGTGTGAGCGAGGCG 533
Db |||||
365 CGGACACACGCTGAGTCGACATGAAGCACTGGCCCTTCAGAGTGTGAGCGAGGCG 424
QY 534 GCAAGCCAAAGTGCAGTATGTCTACCGCGGAGGACAGAGCTTCTACCCCGAGGAGA 593
Db |||||
425 GCAAGCCAAAGTGCAGTATGTCTACCGCGGAGGACAGAGCTTCTACCCCGAGGAGA 484
QY 594 TCTCGTCCATGCTGAGCAAGATGAAGGAGACGGCCGAGGGGTACCTGGGCGAGCCCG 653
Db |||||
485 TCTCGTCCATGCTGAGCAAGATGAAGGAGACGGCCGAGGGGTACCTGGGCGAGCCCG 544
QY 654 TGAAGCAGCAGTATCAGCGTG 676
Db |||||
545 TGAAGCAGCAGTATCAGCGTG 567

RESULT 12

DA828714
LOCUS
DEFINITION DA828714 PLACE1 Homo sapiens cdna clone PLACE1001595 5', mRNA
sequence.
ACCESSION DA828714
VERSION DA828714.1 GI:83046739
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1. (bases 1 to 662)
AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaquri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
HRI.

FEATURES

source
Location/Qualifiers
1..662
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1001595"
/tissue_type="placenta"
/clone_lib="PLACE1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 20.4%; Score 508; DB 9; Length 662;
Best Local Similarity 100.0%; Pred. No. 6.2e-258;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 ATCGGGCGCAAGTTTCGGGACACCGGTGCGAGTCGAGTCGAGCATGAAGCACTGGGCCCTTCCAG 517
Db |||||
1 ATCGGGCGCAAGTTTCGGGACACCGGTGCGAGTCGAGTCGAGCATGAAGCACTGGGCCCTTCCAG 60
QY 518 GTGTGTGAGGAGGCGGCAAGCCCAAGGTGCGCGTATGCTACCGGGGGAGGACAAGCG 577
Db |||||
61 GTGTGTGAGGAGGCGGCAAGCCCAAGGTGCGCGTATGCTACCGGGGGAGGACAAGCG 120
QY 578 TTCTACCCCGAGAGATCTGTCCTCATGTGCTGAGCAAGATGAAGGAGACGGCGGCGG 637
Db |||||
121 TTCTACCCCGAGAGATCTGTCCTCATGTGCTGAGCAAGATGAAGGAGACGGCGGCGG 180
QY 638 TACCTGGGCGACCGCGTGAAGCACGCGAGTCACCGTCCCACTATTTCAAGTAAGTCG 697
Db |||||
181 TACCTGGGCGACCGCGTGAAGCACGCGAGTCACCGTCCCACTATTTCAAGTAAGTCG 240
QY 698 CAGCGCGAGGCCACCAAGGACCGGGGGCCATCGGGGGCTCAAGGTGTCGCGATCATC 757
Db |||||
241 CAGCGCGAGGCCACCAAGGACCGGGGGCCATCGGGGGCTCAAGGTGTCGCGATCATC 300
QY 758 AATGAGGCCACGCGAGCGCATCCCTATGCGCTGAGCCGCGGGCGCGGGAAGCGC 817
Db |||||
301 AATGAGGCCACGCGAGCGCATCCCTATGCGCTGAGCCGCGGGCGCGGGAAGCGC 360
QY 818 AACGTGCTCATTTTTGACCTGGGTGGGGCACCTTCGATGTGTCGTTCTCTCCATTGAC 877
Db |||||
361 AACGTGCTCATTTTTGACCTGGGTGGGGCACCTTCGATGTGTCGTTCTCTCCATTGAC 420
QY 878 GCCGTGTCTTTGAGGTGAAGCCCACTGCTGGAGATACCCACTGGGAGGAGGACTTC 937
Db |||||
421 GCCGTGTCTTTGAGGTGAAGCCCACTGCTGGAGATACCCACTGGGAGGAGGACTTC 480
QY 938 GACAAACCGGCTCGTCAACCACTTCATGG 965
Db |||||
481 GACAAACCGGCTCGTCAACCACTTCATGG 508

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RESULT 13
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LOCUS
DEFINITION BQ212261 852 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7675912 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6095753
5', mRNA sequence.
ACCESSION BQ212261
VERSION BQ212261.1 GI:20392319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLA13368 row: k column: 18
High quality sequence stop: 589.
Location/Qualifiers
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/clone_lib="NIH_MGC_72"
/node="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
FEATURES
source
1..852
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
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/node="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 20.2%; Score 503; DB 3; Length 852;
Best Local Similarity 99.8%; Pred. No. 2.9e-255;
Matches 553; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 300 TTCAGCAGGCGCGTGGAGATCCTGGCCAAACGACGAGGCAACCGCCAGCCAGCCAGCT 359
DB 1 TTCAGCAGGCGCGTGGAGATCCTGGCCAAACGACGAGGCAACCGCCAGCCAGCT 60
QY 360 ACCTGGCCCTTACCGACACGAGCGGCTGGTGGGGAACGCGCCAGAGCCAGCGGCC 419
DB 61 ACCTGGCCCTTACCGACACGAGCGGCTGGTGGGGAACGCGCCAGAGCCAGCGGCC 120
QY 420 TGAACCCCAACACACCGTGTTCGATGCCAGCGGCTGATCGGCGCAAGTTCCGCGACA 479
DB 121 TGAACCCCAACACACCGTGTTCGATGCCAGCGGCTGATCGGCGCAAGTTCCGCGACA 180
QY 480 CCACGGTGCAGTCGGACATCAAGCATCTGGCCCTTCACAGGTGGTGAAGCGGCGGCAAGC 539
DB 181 CCACGGTGCAGTCGGACATCAAGCATCTGGCCCTTCACAGGTGGTGAAGCGGCGGCAAGC 240
QY 540 CCAAGGTGCGGTATGTATCCCGGGGAGGACGAAGAGCTTACCCCGAGGAGACTCGT 599
DB 241 CCAAGGTGCGGTATGTATCCCGGGGAGGACGAAGAGCTTCTACCCCGAGGAGACTCGT 300
QY 600 CCATGGTGTGAGCAAGATCAAGAGACGCGCCAGAGCGTACCTGGGCCAGCCCGTGAAGC 659
DB 301 CCATGGTGTGAGCAAGATCAAGAGACGCGCCAGAGCGTACCTGGGCCAGCCCGTGAAGC 360
QY 660 ACGCAGTGATCACCGTCCCACTTATTTTCATGTAATCTCGACGCGCCAGGCCACCAAGGAG 719

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DB 361 ACGCAGTGATCACCGTGGCCACCTATTTCAGTAACTCGCAGCGCGCCACCAAGGAGC 420
QY 720 CGGGGGCCATCGCGGGGCTCAAGTGCTGCGGATCATCATGAGGCCACGCGCAGCGCA 779
DB 421 CGGGGGCCATCGCGGGGCTCAAGTGCTGCGGATCATCATGAGGCCACGCGCAGCGCA 480
QY 780 TGGCTATGGGCTGACCGCGGGCGGGGAAAGCGCAACGCTGCTCATTTTTCACCTGG 839
DB 481 TGGCTATGGGCTGACCGCGGGCGGGGAAAGCGCAACGCTGCTCATTTTTCACCTGG 540
QY 840 GTGGGGGACACCTTC 853
DB 541 GTGGGGGACACCTTC 554

RESULT 14
AI636649/c
LOCUS
DEFINITION AI636649 575 bp mRNA linear EST 14-DEC-1999
ts92b11.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2238717 3'
similar to gb.X51757_cde1 HEAT SHOCK 70 KD PROTEIN 6 (HUMAN);, mRNA
sequence.
ACCESSION AI636649
VERSION AI636649.1 GI:4687979
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 575)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 616 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 443.
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plasmid DNA from the normalized library NCI CGAP GC4 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1257096-1258631, 1469064-1470963, and
1475592-1476743). Subtraction by Bento Soares and M.
Fatima Bonaldi."
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purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1257096-1258631, 1469064-1470963, and
1475592-1476743). Subtraction by Bento Soares and M.
Fatima Bonaldi."
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RESULT 15

BX348810

LOCUS

DEFINITIONBX348810 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

ACCESSIONBX348810

VERSIONBX348810.2

KEYWORDSGI:46554426

SOURCEEST.

ORGANISMHomo sapiens (human)

REFERENCE1 (bases 1 to 877)

AUTHORSLi, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLEFull-length cDNA libraries and normalization

JOURNALUnpublished (2001)

COMMENTOn May 5, 2003 this sequence version replaced gi:30383328.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

1112.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0BAG028ZB11_CS02674_1&c=1112.f

FEATURES

source

Location/Qualifiers

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	502	20.1	2279	5	BC035665	BC035665 Homo sapi
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7	495	19.9	129505	5	AL590385	AL590385 Human DNA
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ALIGNMENTS

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DEFINITION		Homo sapiens (human)				
ACCESSION		Homo sapiens				
VERSION		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
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SOURCE		Parsian,A.J., Sheren,J.E., Tao,T.Y., Goswami,P.C., Malyapa,R., Van Rheeden,R., Watson,M.S. and Hunt,C.R.				
ORGANISM		The human Hsp70B gene at the HSPA7 locus of chromosome 1 is transcribed but non-functional				
REFERENCE		Biochim. Biophys. Acta 1494 (1-2), 201-205 (2000)				
AUTHORS		11072087				
TITLE		2 (bases 1 to 2493)				
JOURNAL		Hunt,C.R., Malyapa,R., Parsian,A.J., Goswami,P.C., Van Rheeden,R. and Watson,M.S.				
PUBMED		Direct Submission				
AUTHORS		Submitted (22-SEP-1998) Radiation Oncology, Washington University School of Medicine, 4511 Forest Park Blvd., St. Louis, MO 63108, USA				
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Mon Nov 6 11:55:55 2006

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Qy	2221	TCTTCTATGATCCCTGCTTCAGAGATGAAGGGCTTGGGGGGTCTTCCCTCCAAAGCTA	2280
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Qy	2341	TCTTCTGCTTCAATAAAGTCAATTAATTAATAAAGTGTGTGCACTTAAACATTG	2400
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AL451067			

LOCUS DEFINITION

Human DNA sequence from clone RP11-25K21 on chromosome 1, complete sequence.

ACCESSION

AL451067 AC031995

VERSION

AL451067.12 GI:62177046

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 150019)
Barlow, K.

TITLE

Direct Submission

JOURNAL

Submitted (02-APR-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Apr 2, 2005 this sequence version replaced gi:62148838.
Draft Sequence Produced by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
http://www.seq.wi.mit.edu

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
RP11-25K21 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.

FEATURES

source

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2492; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGGGGGGGGGGGGGGTCTCGACTGGGGGGGAAGTTCGGGAAGTTTCGGGGG 60
|||||
Db 70759 CCGGGGGGGGGGGGGGGGGTCTCGACTGGGGGGGAAGTTCGGGAAGTTTCGGGGG 70818

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QY	301	TCAGCAGGCGCGTGGAGATCTTGGCCAAACGACGAGGCAACCGCACACGCGCCAGCTA	360	Db	72139	TGGGGGCAAAATGTGAGAAAGTGCAGGATCTCTCTGCTGATGTGCTCCCTGTCTC	72198
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Db	71239	CAGGTGCACTCGGACATGAAGACCTGCGCCCTTCAGGTGTGAGCGAGGGCGCAAGCC	71298	QY	1621	TCATTGGCATCCCTCTGCCCCACATGGAGTCCCCAGATAGAGGTGAGTTTGACATTG	1680
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QY	961	CATGGAGAAATCCGCGGAGCATGGGAAGACCTGAGCGGGGAAACAGCGTGCCTGGG	1020	Db	72799	GTCCGCCCATCTTCTCCAGGCTCTATGGGGGCGCTGGTGTCCCTGGGGGACAGTTGTA	72858
Db	71719	CATGGAGAAATCCGCGGAGCATGGGAAGACCTGAGCGGGGAAACAGCGTGCCTGGG	71778	QY	2101	GCCTCAGCCACAGGGGACCCCGCAGCAGCGGGCCCATATTGAGAGGTTGATTGAA	2160
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VERSION CQ730982.1 GI:42306299
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
AUTHORS Kits, such as nucleic acid arrays, comprising a majority of
TITLES humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16916 06-SEP-2002;
PE Corporation (NY) (US)
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RESULT 5
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LOCUS
DEFINITION Homo sapiens heat shock 70kDa protein 6 (HSP70B'), mRNA

BC035665 2279 bp mRNA linear PRI 09-DEC-2005
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REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1. (bases 1 to 2279)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klautner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Uadin,T.B., Toshlyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Woreley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSTRM	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2. (bases 1 to 2279)
AUTHORS	NH MGC Project
CONSTRM	Direct Submission
TITLE	Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
JOURNAL	NH-MGC Project URL: http://mgc.nci.nih.gov
REMARK	Contact: MGC help desk
COMMENT	Email: gcaps@emil.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhi.nih.gov Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.I., Masiello,C., Maeskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 79 Row: 9 Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 42822885. Location/Qualifiers 1..2279 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:46216 IMAGE:5723718" /cissue_type="Ovary, pooled from 3 adults" /clone_lib="NH_MGC_125"

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Db 851 CGGCGGAAGCATGGGAAGGACTGAGCGGGAAACAAAGCGTGCCTGCGCAGGCTCGGCACA 910
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RESULT 6
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LOCUS Homo sapiens mRNA for heat shock 70kDa protein 6 (HSP70B') variant,
DEFINITION clone: FCC101B10. 2318 bp mRNA linear PRI 26-APR-2005
ACCESSION AK223362
VERSION AK223362.1 GI:62898284
KEYWORDS FLI_CDNA; oligo capping.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1

AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS
COMMENT
FEATURES
source
CDS
ORIGIN

Maruyama,K. and Sugano,S.
Oligo-capping: a simple method to replace the cap structure of
eukaryotic mRNAs with oligoribonucleotides
Gene 138 (1-2), 171-174 (1994)
8125298
2
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S.
Construction and characterization of a full length-enriched and a
5'-end-enriched cDNA library
Gene 200 (1-2), 149-156 (1997)
9373149
3 (bases 1 to 2318)
Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A. and
Yokoyama,S.
Direct Submission
Submitted (22-APR-2005) Akiko Tanaka, RIKEN Yokohama Institute,
Protein Research Group; 1-7-22 Suehiro, Tsurumi, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:aktanaka@riken.jp,
URL: http://protein.gsc.riken.jp/, Tel:81-45-503-9452,
Fax:81-45-503-9450)
This work was supported in part by the National Project on Protein
Structural and Functional Analysis, Ministry of Education, Culture,
Sports, Science and Technology of Japan.
Location/Qualifiers
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DVLVVGGSFRIIPKVQKLQDFNFKELNKSINPDEAVAYAAVQAAVLMGDKCKEVQD
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Query Match 19.9%; Score 495; DB 5; Length 2318;
Best Local Similarity 99.8%; Pred. No. 8e-286;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 134 GCAGAGAAACCGCAGGAGAGGCTCTCACTGCTGAGCGCCCTCGACCGCGGAGCGGAGCA 193
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Qy 254 GCGGTGGGATGACCTGGGACCACTACTCGTGGTGGGCGGTGTTTCAGCAGGCGCCG 313
Db 141 GCGGTGGGATGACCTGGGACCACTACTCGTGGTGGGCGGTGTTTCAGCAGGCGCCG 200
Qy 314 GTGAGATCCTGGCCAAACGACGAGGGGCAACCGCACCGCCAGCTACGTGGCGCTTCACC 373

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, one subclone, and the assembly was done being a YAC.

FEATURES

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misc feature

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Db	561	GTGCCC	566		
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DEFINITION	Human DNA sequence from clone Rp11-5K23 on chromosome 1. Contains the FCGR2A gene for Fc fragment of IgG low affinity IIA receptor for (CD32), the HSPA6 gene for heat shock 70kDa protein 6 (HSP70B), a ribosomal protein S23 (RPS23) pseudogene, the FCGR3A gene for Fc fragment of IgG low affinity IIA receptor for (CD16), a novel gene and three CpG islands, complete sequence.				
ACCESSION	AL590385	AC013307			
VERSION	AL590385.23	GI:48374143			
KEYWORDS	HTG; FCGR2A; FCGR3A; HSPA6; RPS23.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 129505)				
AUTHORS	Lovell, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk				
COMMENT	Clone requests: clonerequest@sanger.ac.uk On Jun 6, 2004 this sequence version replaced gi:21211764. Draft Sequence Produced by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA http://www-seq.wi.mit.edu The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 Rp11-5K23 is from the library RPI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAC3.6 ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk				

[illegible]

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Query Match 19.9%; Score 495; DB 5; Length 129505;
Best Local Similarity 99.8%; Pred. No. 7.3e-286;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	374	GACACCGAGCGGTGGTTCGGGCAACGGCGCAAGAGCCAGGGCGCCCTCGAACCCCAAC	433
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Qy	434	ACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGCAACACCGTGCAGTCG	493
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Qy	494	GACATGAGCACTGGGCCCTTCAGGTGTGACGAGGGGGCAAGCCCAAGTGGCGGTA	553
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Qy	554	TGCTACCGGGGAGGACAAGACGTTCTACCCCGAGGAGATCTCGTCCATGCTGCTGACG	613
Db	81639	TGCTACCGGGGAGGACAAGACGTTCTACCCCGAGGAGATCTCGTCCATGCTGCTGACG	81698
Qy	614	AAGATGAGGAGACGGCCGAGCGTACCTGGGCGAGCCCGTGAAGACGACGAGTGATCACC	673
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RESULT 8
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ACCESSION AR531647
VERSION AR531647.1
KEYWORDS GI:53920086
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2336)
AUTHORS Kaser, M.R.
TITLE Genes expressed in treated human C3A liver cell cultures
JOURNAL Patent: US 6727066-A 203 27-APR-2004;
Incyte Corporation; Palo Alto, CA
FEATURES Location/Qualifiers

RESULT 8	REFERENC	FEATURES
AR531647	AUTHOR	
LOCUS	TITLE	JOURNA
DEFINITI		
ACCESSION		
VERSION		
KEYWORDS		
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QY	1352	TGGGTCTGCTGTCAGCGCGCGCTGTGATGGGGGACAAATGTGAGAAAGTGCAGGATCT	1411
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DB	1288	CCTGCTCTCGATGTGGCTCCCTGTCCTGCGGCTGGAGACAGCAGCTGGGTGATGAC	1347
QY	1472	CACCTGATCCAGAGGAAGCCCACTATCCCAAGCAGACCCAGACTTTCACACCTA	1531
DB	1348	CACCTGATCCAGAGGAAGCCCACTATCCCAAGCAGACCCAGACTTTCACACCTA	1407
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LOCUS	Homo sapiens cDNA FLJ36606 fis, clone TRACH2015654, highly similar		
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ACCESSION	AK093925		
VERSION	AK093925.1	GI:21752885	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishio, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosori, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamiyama, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Tanai, H., Kimata, M., Watanabe, M., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosiida, M., Hotta, Y., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., O., Nomura, Y., Imose, N., Musashino, K., Yuki, H., Oshima, R., Takeuchi, K., Arita, M., Imose, N., Yohikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Satoh, N., Takami, S., Shiohara, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terasima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Watanabe, T., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikemura, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Itoh, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,		

Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Moniyama, H., Onogawa, S., Kasriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Kataoka, K., Kuga, N., Kuroda, A., Satoh, I., Kanata, K., Takami, S., Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsumoto, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagaesuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 2253)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: flj-cdna@ifty.com, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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DB 81 GCCTCGGTGGCTCCAGCATCCGACAGAGCTTCAGCCATGACGAGCCCGCCACGGGAGCTC 140
QY 254 CGGGTGGGATCACTGGGCGACACCTACTCTGCTGGGGCGGTGTTTACGAGGGCCCGC 313
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QY 314 GTGGAGATCTGCGCAACGACGAGGCAACCGCACCGCCAGCGCTACGTGGCTTCACC 373
DB 201 GTGGAGATCTGCGCAACGACGAGGCAACCGCACCGCCAGCGCTACGTGGCTTCACC 260
QY 374 GACACGAGCGGTGGTTCGGGAGCGGGCGCAAGAGCGAGCGGCGCTTGAACCCCAACAC 433
DB 261 GACACGAGCGGTGGTTCGGGAGCGGGCGCAAGAGCGAGCGGCGCTTGAACCCCAACAC 320
QY 434 ACCGTGTTGATGCCAAGCGGCTGATCGGCGCGCAAGTTTCGGGACACCAACCGTGCAGTCG 493

Db 321 ACCGTGTTGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACACACCGTGCAGTCG 380
QY 494 GACATGAGCACTGGCCCTTCAGGTGTTGAGCGGGCGGCAAGCCCAAGGTGCGCGTA 553
Db 381 GACATGAGCACTGGCCCTTCAGGTGTTGAGCGGGCGGCAAGCCCAAGGTGCGCGTA 440
QY 554 TGCTACCGCGGGGAGGACAAAGACGTTCTACCCCGGAGGAGATCTCGTCCATGGTGTGAGC 613
Db 441 TGCTACCGCGGGGAGGACAAAGACGTTCTACCCCGGAGGAGATCTCGTCCATGGTGTGAGC 500
QY 614 AGATGAGGAGACGCGCGGCGGCTACCTGGGCGGAGCCCGCTGAAGCAGCAGTGATCACC 673
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QY 674 GTGCC 679
Db 561 GTGCC 566

RESULT 10
BX537284
LOCUS
DEFINITION
Homo sapiens chromosome 1 clone XX-86542C10, 2 unordered pieces.
BX537284
VERSION
BX537284.3 GI:32134910
HTG; HTGS PHASE1; HTGS_CANCELLED.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 136035)
Glicthero.R.
Direct Submission
Submitted (19-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jun 20, 2003 this sequence version replaced gi:31620806.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: fw86542C10
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 32214 bases at least Q40
Consensus quality: 32390 bases at least Q30
Consensus quality: 36787 bases at least Q20
Insert size: 135335; sum-of-contigs
Insert size: 38793; 21.5% error; agarose-fp
Quality coverage: 10.50x in Q20 bases; sum-of-contigs Quality coverage: 38.74x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 107755: contig of 107755 bp in length
* 107756 107755: gap of 100 bp
* 107756 136035: contig of 28180 bp in length.
Location/Qualifiers
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Best Local Similarity 99.6%; Pred. No. 4.6e-255;
Matches 544; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 134 GCAGAGAAACCGCAGGAGAGCCTCACTGTCAGCGCCCTCGACGGCGGAGCGGACCA 193
Db 106478 GCAGAGAAACCGCAGGAGAGCCTCACTGTCAGCGCCCTCGACGGCGGAGCGGACCA 106537
Qy 194 GCCTCCGTGGCCTCCAGCATCCGACAGAAAGCTTCAGCCATGAGGCCCCACGGGAGCTC 253
Db 106538 GCCTCCGTGGCCTCCAGCATCCGACAGAAAGCTTCAGCCATGAGGCCCCACGGGAGCTC 106597
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Db 106718 GACACCGAGCGGTGTTCGGGAGACCGGCAAGAGCGGCGCCCTGAACCCCCCAAC 106777
Qy 434 ACCGTGTCGATGCCAAGCGGTGATCGGGCGCAAGTTTCGGGACACACCGTGCATCG 493
Db 106778 ACCGTGTCGATGCCAAGCGGTGATCGGGCGCAAGTTTCGGGACACACCGTGCATCG 106837
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Db 106838 GACATGAAGCACTGGCCCTTCAGGTGTGAGCGGCGGCAAGCCCAAGTTCGGGTA 106897
Qy 554 TGTACCGCGGGAGGAGACGTTCTACCCCGAGGAGATCTCGTCCATGTTGCTGAGC 613
Db 106898 TGTACCGCGGGAGGAGACGTTCTACCCCGAGGAGATCTCGTCCATGTTGCTGAGC 106957
Qy 614 AAGATGAAGGAGACGCGCCGAGGCGTACCTGGGCGCAGCCGTTGAACGACGAGTATCACC 673
Db 106958 AAGATGAAGGAGACGCGCCGAGGCGTACCTGGGCGCAGCCGTTGAACGACGAGTATCACC 107017
Qy 674 GTGCCC 679
Db 107018 GTGCCC 107023

RESULT 11
AR454599 2962 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 72 from patent US 6682888.
DEFINITION AR454599
ACCESSION AR454599
VERSION AR454599.1 GI:42688068
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2962)
Loring,J.F., Tingley,D.W. and Edwards,C.M.
Genes expressed in alzheimer's disease
Patent: US 6682888-A 72 27-JAN-2004;
Incyte Corporation; Palo Alto, CA
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/mol_type="genomic DNA"

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Best Local Similarity 99.8%; Pred. No. 3.6e-247; Indels 0; Gaps 0;
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Qy 258 TGGGCATCGACCTGGGCAACCACTACTCGTGGTGGGCGTGTTCAGCAGGGCGCGTGG 317
Db 759 TGGGCATCGACCTGGGCAACCACTACTCGTGGTGGGCGTGTTCAGCAGGGCGCGTGG 818
Qy 318 AGATCTGGCCACGACGAGGCAACCGCACCGCCAGCTACGTGGCCTTCACCGACA 377
Db 819 AGATCTGGCCACGACGAGGCAACCGCACCGCCAGCTACGTGGCCTTCACCGACA 878
Qy 378 CCGAGCGGCTGTTCGGGACCGCGCCAAAGAGCGGCGGCGCTGAACCCCAACACCG 437
Db 879 CCGAGCGGCTGTTCGGGACCGCGCCAAAGAGCGGCGGCGCTGAACCCCAACACCG 938
Qy 438 TGTTCGATGCCAAGGGCTGATCGGGCGCAAGTTTCGGGACACACCGTGCAGTCGACA 497
Db 939 TGTTCGATGCCAAGGGCTGATCGGGCGCAAGTTTCGGGACACACCGTGCAGTCGACA 998
Qy 498 TGAAGCACTGGCCCTTCAGGTGTGAGCGGCGGCAAGCCCAAGTTCGGCTATGCT 557
Db 999 TGAAGCACTGGCCCTTCAGGTGTGAGCGGCGGCAAGCCCAAGTTCGGCTATGCT 1058
Qy 558 ACCGGGGAGAGCAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGTTGCTGAGCAAGA 617
Db 1059 ACCGGGGAGAGCAAGAGCTTCTACCCCGAGGAGATCTCGTCCATGTTGCTGAGCAAGA 1118
Qy 618 TGAAGGAGACGCGCGGCGGTACCTGGGCGACCCGTTGAAGCAGCAGTATCACCCTGC 677
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Qy 678 CC 679
Db 1179 CC 1180

RESULT 12
BV198650 401 bp DNA linear STS 10-JUN-2004
LOCUS sgml198410 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV198650
VERSION BV198650.1 GI:48166754
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 401)
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.N. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press
JOURNAL
COMMENT
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 401
Location/Qualifiers

FEATURES
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QY	2083 CTGGGGGAGCAGTTGTAGGCTTAAGCCCACACAGGGGACCCCAAGACCCTCA	TCA 2142			
Db	181 CTGGGGGAGCAGTTGTAGGCTTAAGCCCACACAGGGGACCCCAAGACCCTCA	TCA 240			
QY	2143 TTGAGAGGTTGATTGAAATGGCCCTCGTGATAAGTTCAGCTGTGACTTCAGGG	CTATGC 2202			
Db	241 TTGAGAGGTTGATTGAAATGGCCCTCGTGATAAGTTCAGCTGTGACTTCAGGG	CTATGC 300			
QY	2203 TATGGGCTTCTAGACTGTCTTCTATGATCTCGCCCTTCAGAGATGAAGGG	CTTGGGGGG 2262			
Db	301 TATGGGCTTCTAGACTGTCTTCTATGATCTCGCCCTTCAGAGATGAAGGG	CTTGGGGGG 360			
QY	2263 GTCTTCCCTCCAAGCTAGAACCTTTCTTCCAGGATAACTG	2303			
Db	361 GTCTTCCCTCCAAGCTAGAACCTTTCTTCCAGGATAACTG	401			
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S78631	LOCUS	HSPA6=70-kda heat-shock protein [human, Genomic, 1001 nt].	PRI 07-MAY-1993		
DEFINITION	S78631	linear			
ACCESSION	S78631				
VERSION	S78631.1	GI:244243			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1001) Leung,T.K., Hall,C., Rajendran,M., Spurr,N.K. and Lim,L. The human heat-shock genes HSPA6 and HSPA7 are both expressed and localize to chromosome 1 Genomics 12 (1), 74-79 (1992) PUBMED 1346391 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsg 78631] from the original journal article.				
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487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 15
 HSP70B
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 DEFINITION
 ACCESSION X51757
 VERSION X51757.1 GI:35221
 KEYWORDS heat shock protein; heat shock protein 70; heat shock protein
 HSP70B; hsp70B gene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo
 1 (bases 1 to 2492)
 Leung,T.K., Rajendran,M.Y., Monfries,C., Hall,C. and Lim,L.
 The human heat-shock protein family. Expression of a novel
 heat-inducible HSP70 (HSP70B) and isolation of its cDNA and
 genomic DNA
 Biochem. J. 267 (1), 125-132 (1990)
 2327978
 2 (bases 1 to 2492)
 Rensing,S.A. and Maier,U.G.
 Phylogenetic analysis of the stress-70 protein family
 J. Mol. Evol. 39 (1), 80-86 (1994)
 7545947
 3 (bases 1 to 2492)
 Hall,C.
 Direct Submission
 Submitted (01-FEB-1990) Hall C., Institute of Neurology, Dept of
 Neurochemistry, 1 Wakefield Street, London WC1N 1PU, UK
 See <X51758> for partial HSP70B' cDNA.
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 Best Local Similarity 100.0%; Pred. No. 1.4e-185; Indels 0; Gaps 0;
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